

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

CCAGGTCCAAACCTGCACCTCGGTTCTATCGATTGGAATTCCTCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCTCCAGCGGCCAGTGGGCTTGAGGCCACG  
AAGGGCTAGGGTTCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCTCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGTGTTTGGCAGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC  
CGCCGCGAGCCCTGGGCTGGCCCTTGCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAG  
GACACGCGGGCTTCTCTGGGCTGTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAAACGGAG  
GGAGCTGTGTGCAGCCTGGCCGTGCGGCTGCGGCTGCAGGATGGCGGGGTGCACACTTGCAC  
TCAGATGTGTGAGCTGAATGCAGTGTAGGAGGGCGCGCTGTCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGTTGCCAGTGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGTCACAGCCTGGCCTCGCAGGCACCTGGAGCATGGGCTCCCGGACCCCGCAGCC  
TCCTGGTGCACCTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC  
CTGGAGGAGCAGCTGGGGTCTGCTCTCTGCAAGAAAGACTCGTGACTGCCACGCGCCCCAGG  
CTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTTCTCTCTC  
CCCTTCCCTCGGGAGGGTCCCCAGACCTTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCTGTGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCTCAGTGGGGGCTGTGCTGCCTGACCCCCAGCACAAATAAAATGAAA  
GTGAGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCT  
AGATCGAACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCACTTATAATGGT  
TACAAT

## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCPVKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

100705035.101604

### FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCCACGGCGGGGACTATGGTGAATAATCCCGGCGCTCACGCACTACTGGCCCCGTATC  
CGGTTCTTTGGTGCCCTTGGGCATACCAACATAGCCATCGACTTCGGGGAGCAGGCGCTTGAA  
CCGGGGCATTGTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTCTTCCACGGGTCCCATGAGTGACTTCAAAAAATGTGGGCCCTGGTGTT  
GTGAACAGCAGAGAGACAGGACCAAGCCGTCTCTGTATGTGGTGGCGAGGGCCATCGC  
TGCCGTCTTTACACACTGATAGCTTATAGTGATTAGGATACTACATTATCAATAAACATGCG  
ACCATGTGGACAGTTCGGTGGGGAGCAAGACGAGAAGGGCCTCTGCTACCTCGCGCCCTTT  
CCTTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACAAATACAGTTT  
CCTGGTGGGATGTGCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCCGGGAGCCCTGCTCATCCGATCCTCCTTGATACATGGGC  
GCACTTGTGCGCTGCACCACCTGTGCTGGGCTACTACAAGAACATTCCAGCATCATCCC  
TGACAGAAGTGGCCCGGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCATTCTGCAGCCACAGAGGCAGTGGCGGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCTCAATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCTCTGTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCAGCAGCAACAGTCACGGCAGGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCAGCTCTGTTTTCGTGATGTTTGGAC  
ACCCAAAGCTGTCTGAGAAAACTTGTATAGACATCATCGGAGTGGAGTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCCCTTGGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT  
CTCACCGGCTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTCG  
GATCATCGTCTCATCGCCAGCCTCGTGGTCTACCTACTGGGGGTGCACGGGTCGAGCCC  
TGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGTCGCGCATCGCTCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA  
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAG  
AGAATGAATAAGGCACGGGAGCCCATGGGCACTGCAGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTGTGTTTGTGTTGGTAAT  
GAAAGAGGCTTGTATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACT  
GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC  
TTCATACCCCTGCCTACGAAAAACCAAAAGACACAGCTGCCCTACCGTTGACGTTGTGTCC  
TCCTCCCTGGACAATCTCTCTTGGAAACAAAGGACTGCAGCTGTGCCATCGCGCTCGGT  
CACCTGTCACAGAGGCCACAGACTCTCCTGTCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAACTCGGCTTCCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCAGCGCTGCAGCCCGGAGTCCCGTTACACCTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAAATCTCCGTAAGAAAGGTTTGGTTTGAATGCCCCGG  
GGCAGCAACTGACATGGTTGAATGATAGCATTTCACTCTGCTCTCTAGATCTGAGCAA  
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTTGTCAAAAA  
GCGCATCTCCAGATTCAGACCTTGCCTGCGCATGACTTTTCTGAAAGGCTTGCTTTTCCCTCGC  
CTTTCTGAAAGTTCGATTTAGAGCGAGTCACATGGAGCATCTCACTTTGCTATTTGTTT  
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAA  
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGTAATTTCCCTCCACACCATAGATCAAGCAAGACATTTATAACG  
ATACCAGAGTCACATATGTGGTCTCCCTGAAATAACGCATTGAAATCCATGCAGTGCAGTA  
TATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTAAAAAATATAGACACGGTCTCACT  
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTTCTATTTTCGC  
ATTTTCAATAAAATGTCTTAATCAAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSEDFKNVGLVFNNSKRDRTKAVLCMVVAGATAAVFHTLIAYSDLGYIINKLHHVDESV  
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQRI SRPIVNL FVS RDLGGSSAATEAVAILTATYPVGHMPYGLTEIRAVYPAFDKNNPSN  
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR  
IFSFFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRRIIVLIASLVVLPYLGvHGATLGvGSLL  
AGFVGESTMVAIAACYVYRKQKKKMENESATEGEDSAMTDMPTTEEVTDIVEMRENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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CCTGACAGAAGTGCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
 GCCNITTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
 TCCCGGGACCTTGGTGGCAGTTCTGCAGGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
 CCCTGTGGGTCAATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCTGCTTTTCG  
 ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGCGGCCCCACATC  
 AAGAAGTTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTGGAC  
 ACCCAAGTCTGTTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
 TCTCGTGTGTTCTTTGCGGATCTTCTCTCTCCAGTCCAGTCACAGTGAAGGCGCAT  
 CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTGTC

## FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT  
CCTTTTTCCCAGTTCAGTCACAGNGAGGGCGCATCTCACCGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCAGCTNNTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCTACCTGGGGGTGCACGGTGCGACCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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## FIGURE 7

TATTC C CAGTTC C GGT C A C G G G G A G G G C G C A T N T C A C C G G G T G G C T G A N G A C A C T G A A G A A A  
A C C T T N G T C C T T G C C C C C A G N T T T G T G N T G C G G A T N A T C G T C C T C A T C G C C A G C C T N G T G G T  
C C T A C C C T A C C T G G G G G T G C A C G G T G A G A C

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## FIGURE 8

GCCTGCTCCCTGCTCAGTGCAGCGTCTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGCGTGGAGAGTCACTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGCGCGGATCCCAACCGTCTTCGAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGCGCGCCTTCTTCTTCT  
TCTTTTTCACCCGTCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGGGCTCCTTCTCTTCA  
TCCTCATCCAGCTGGTGTCTCATCGACTTTGCGCACTCCTGGAACAGCGGTGGCTGGGC  
AAGCCGAGGAGTGCATTCCCGTGCTGGTACGCAAGGCTCTTCTTCTTCACTCTCTCTT  
CTACTTGTCTGCATCGCGGCGTGGCGCTGATGTTTATGTACTACACTGAGCCACGCGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTTCTGTGCTTGCCTGTCATCGCT  
GCTGTCTGCCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCTCGGTGAT  
CACCCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCGAGCATTTGTGGGCTCATCATCTTCTCTGTGCACCCCTCTT  
CATCAGTCTGCGTCTCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACTACAGCTACTCTTCTTCCACTTCTGCTTGGTGCT  
GGCCTCACTGCACGTGATGATGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCGGTGGGTGAAGATCTGTGCCAGCTGGGCAGGCTGCTCTCTC  
TACCTGTGGACCTTGGTAGCCCCACTCTCTTGCGCAACCGGACTTCAGCTGAAGGACGCT  
CACAGCCTGCCATCTGGTGCTCTTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCTTCTAGTCTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCTTGCA  
GAGCCCCATCCCCCGCCACACCCACAGGTGGAGCTGCCCTTCTTCCCTTCCCTCTCTCTGT  
TGCCATACTCAGCATCTCGATGAAAGGGCTCCCTTGCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGAACTCCACACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT  
CCTGGTCACGTCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAAACAAGCCAGTGCCTGTAACAAAAA



## **FIGURE 9**

MGACLGACSLSCASCLCGSAPCILSCCCPASRNSTVSRIFTFFFLFLGVLVSIIMLSPGVE  
SOLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLILIQVLVLLIDFAHSW  
NQRWLKAEEDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFIISLNLTFC  
VCVSIAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATOQQQQQVA  
ACEGRAFDNEQDGVITYSYSPFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCGCGGCACGTCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAAGTTTGTCCGTAGGTGAGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGTGTCGGAAGCTG  
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCAGAGCCC  
TATTACCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATGCAGGA  
GCTGTACGCGGAAGTCTTTTAGGATAAAACGTAGGCCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCTTAGAAAAC  
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAACTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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## **FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318  
><subunit 1 of 1, 285 aa, 1 stop  
><MW: 32190, pI: 9.03, NX(S/T): 2  
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEBIYHNRFDVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHPVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENAKKIEALLNLFRNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCAGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGCTTCATG  
GCTGGCGCCGAACC

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### FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

0978585.101604



[illegible]

**Signal Peptide:**

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACC CAAATGACACCTGINTGGCTAGCTGTGTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTNTTCAGTTTTACAGAGATCCTGGGTGTTGGCTGACC  
TACAGATACAGGAACCAG

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## **FIGURE 17**

AATCCCAAATCCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

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## FIGURE 18

ATGATTATTCTGTACTTGTTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

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# FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
 CTCCTGGGTGGCCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
 CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
 TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTG  
 ATCCTCCAAGGTCCAGCCAAGCCAGTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
 CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
 CCGGGCCTAACAGGGAATTCCTCATCACCGTGGTCAAAAGGCAGACAGCGGGCACTACCAC  
 TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCAGAAACAGCATCTGTTGTGGCTAT  
 CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAG  
 CAGGAAGCCCCATGACCTGAGTTGTTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC  
 CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
 CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG  
 ACAACCAAGTTTGGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
 GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACCTGCTCCTGA  
 GGAGGCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
 CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCCTTCTTCAACACATG  
 CAGGATGTGAGAGTCTCTCTCGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
 GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT  
 TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTCTCTGCTCGCACATATGCATAAGTA  
 CTTTACAAAGTTGTCCAGTGTTTGTGTAGAAATAATGTAGTTAGGTGAGTGAATAAAATTT  
 ATATAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
 TGCTGTCTAGATCAGGAATTTCTATCTGTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
 CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
 TTGGGCAATGTTTGAGACATTTTGGTCAATTATCTTGGGGGTTGGGGGATGGTGGGATGT  
 GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCTTATAATGCACAG  
 GGCAGTACCCCAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA  
 CCCCAGCCTAATGAAACCTTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
 TATCTCTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG  
 GTCGTCTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCTTAAATCCCC  
 AAGGTGATGGCATTAAAGAAGTGGGCCCTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
 ATGATTAGGATTAGTGCCCTTATTAAAGGCCCCAGAGAGCTAACTCAACCTTCCACCAT  
 ATGAGGACGTGGCAAGAAATGACATGTATGAGAACCAAAAAACAGCTGTGCGCCAAACACCG  
 ACTCTGTGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAATATGAGAAATAAAATCTGG  
 TTGTTGTAGCCATA

00070505.101601

## FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594  
><subunit 1 of 1, 359 aa, 1 stop  
><MW: 38899, pI: 5.21, NX(S/T): 0  
MKGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPPTPSSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

### **Signal sequence:**

amino acids 1-17

### **Leucine zipper pattern sequence:**

amino acids 12-33

### **Protein kinase C phosphorylation site:**

amino acids 353-355

09573585-103501

# FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAAGTT  
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
 ATCTTACTGGGCTGTACTCTCTGGGCGACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
 GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
 ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAAACGTGGCTCAGACCCCT  
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACAGGGGCCG  
 CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCAAATTGAGCACCCCTGGAGATGG  
 ATGACCCGAGCCACTACACGTGTGAAGTCACTCTGGCAGACTCTCTGATGGCAACCAGTCTGTG  
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCCAAGTGAACAAC  
 TGGCAGCGGTTATGGCTTCAACGGTGCCCCAGGGAATGAGGATTAGCCCTTCAATGCCAGGCTC  
 GGGGTTCTCCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACCCAGGAACCCATC  
 AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
 TTTCTGCACTGCCAAGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
 TCAAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
 TTGAAAGCAACATCTACAGTGAAGCAGTCTGGGACTGGACCACTGACATGGATGGCTACCT  
 TGGAGAGACCAGTGTCTGGGCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCTCATCATCT  
 CTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCGGAAGACATCCCAA  
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCCGT  
 CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAAGACCC  
 AATCCTAAGGCCGGAGGCCTTTCAGGCTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
 CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
 AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAAATTGAGGCAGAGGGGTGGGA  
 AACCAGGACCAAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
 TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGCTGGCCATCTTCGCAAGTGGCTGCT  
 CCAGTGTATGAGCCAACTTCCCAGAACTCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA  
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCTGTCTGGACACAGTTCC  
 TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAATGCCCATTAGGC  
 CAGGATCTGTCTGACATAATTTGCTAGTCACTCTTGCCTTCTGCATGGCCCTTCTTCCCTGCT  
 ACCTCTCTTCTGTGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT  
 GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTCTGGATTGTGGCTCTGG  
 GCCCTTCTAGTATCTCTGCCGGGGCTTCTGGTACTCCTCTCTAAATACCAAGGGGAAGATG  
 CCCATAGCACTAGGACTTGGTCATCATGCTACAGACACTATTCAACTTTGGCATCTTGCCA  
 CCAAGAAGACCCAGGGGAGGCTCAGCTCTGCCAGCTCAGGAGACCAGCTATATCCAGGATCAT  
 TTCTCTTTCTTTCAGGCCAGACAGCTTTAATTGAAATGTATTATTTACAGGCCAGGGTTCA  
 GTTCTGCTCTCCCATATAAGTCTAATGTTCTGACTCTCTCTGGTCTCAATAAATATCTA  
 ATCATAACAGC

0978557.101601

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLFPCTYDPLQGYTQVLVKWLVRGS  
DPVTIIFLRDSSGDHIQQAKYQGRLVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDMGYLGETSAGPGKSLPVFALLIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

09/08/95 10:50:10

**U.S. DEPARTMENT OF AGRICULTURE**

CGCGCGGGAGCCCATCTGCCCCAGGGGACAGGGGCGCGGGGCCGGCTCCGCGCCGGCACAT  
GGCTCGAGCGACCTTCGGCGGACCCCGAGGGCGCCGCGCCAGCTCGCCCGAGGTCCTCGCGGA  
GGCGCCCGCCGCCCGCCGAGCAGACGACCTAGCGGGGAAGCGCCGCTCCGGGGATC  
GGGATGTCCTCTCCTCTCTCTCTTGTCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGGAGAAAGGCTCATTGTGCCCTGCCACATCAACTCGGGGG  
TTCCAGAAAAAGACACTCTGGATATGAATGGCTGCTCACCATAATGAAGGAAACCAAAA  
GTGGTGATCACTTACTCCAGTCTGTCATGTCTACATAACTTGACTGAGGAACCAAGAGGCCG  
AGTGCCCTTTGCTTCCAATTTCTCTGAGGAGATGCCTCTTTCAGATTTGAACCTTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTCTTAAGGTTTAAAGATTCAGGGCGTCACTGTGTGAGCCAT  
GTCACTCTTAAAGTCTTAGTGAGCCATCTCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGAAGGTGACCTGACTTTGAGTGTGAGTCTATCTCGGCACAGAGCCATTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAGAAGGGAGAGGATGAACGCTTGCCTCCAAATCTAGGATT  
GACTACAACCACTTGGACGAGTTCTGCTGCAGAAATCTTACCATGTCTCATCTGGACTGTA  
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAGCTGTGGTGCAGGTAACGTGTACAGT  
ATGTAACAAGCACTCGGATGCTGTGTTCAGGAGCAGTGCAGGCAATAGTGGCTGGAGCCCTGCTG  
ATTTCCTCTTGGTGTGGGTGCTAATTCCGAAGAAAGACAAGAAGATTTAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTTGTGAAACCCAGCT  
CTCTTCTCAGGCTCTCGGAGCTCAGCTCTGGTTCTTCTTCCATCTCGCTCCACAGCAAT  
AGTGCTCTCAGGCAAGCCGAGCACTGTCAACTGACGAGCAACCCAGCCAGGCTGGCCAC  
CGGCATGACAGCTAGTGGGGCCAGAGTGTGAGAGGTTCTGAAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAGCAAAACCAACCCAGCAGCATGATCCCGACGACAGCAGAGCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCACGCTTCTTAGAGTTCAGGGCTTTTGGACTC  
TTCTCGTCACTTGAGCTCAAGTCCAGGCAACCAACCAAGTATGAGAGTCACTTAAGTAGCA  
GTGAGCAITGACGGAACAGATTTCAGATGACATTTCTCTTATCAATACCAACCAAGCAAA  
AGGATTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTTGTGACAGGAGCTGTGGTGAGAAAGGTTGGGGAAAGGTG  
AGGTAATATACCTAAAACTTTAATGTGGGATTTTGTATCATGCTTTGATTCACAATT  
TCAAGAGAAATTTGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTATTGGATT  
ATTAGTATTTCAGACAGTCAAGCAAGCAACCAACGCTTATTACCTGCTACACCATGTAC  
TGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAACATGTGTCCTTCTTATCTGCACTTAAC  
TCTAATTTGATCAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCACTCTACTAATCTCACTCATGTTGTATTGAGCCCAAAATAAC  
TATGAAAGAGACAACAAAATTTGTGACAAAGGATTTGTGACAAAGAGCTTTCATCTTTCATGATGT  
ATGAGGATTGTTGACAAACATTGAAATATATAATGGAGCAATTTGGGATTTTCCCTCAAAAT  
CAGATGCCCTTAAGGACTTCTCTGCTAGATATTTCTGGAAGGAGAAATAACAACATGTCAAT  
TATCAACGCTCTTGAAGAAATTTCTTTCAGAAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATCACTTATAGTCTCTCTTCTTTCAGAAAAATGTGAACACAGAAATGCAAGCATGG  
GTGGACTGAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTGACCGGGCA  
TTGTTCCAGGACCTGTAGGAAAATCCAGCAGGTGTGAGGTTGCAGTGAAGCCGAGATTATGCC  
ATTGCACCTCAGCCTGGGTGACAGAGCGGACTCCGCTCTC

A vertical strip of 12 small, square images showing various stages of a plant's growth, from a seedling to a mature plant.

```
><subunit 1 of 1, 373 aa, 1 stop
```

MSLLLLLLLVSYVVGILGTHTEIKRVAEEKVILPCHHQGLPEKDTLIDIEWLLTDNEGNQKV  
VITYSSRRHVNNLITEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELETGSDTLTQCESSSTEPVIVYVQRIREKEGEDERLPPKSRID  
YNHPRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTQVYQSIGMVAGAVGTIVAGALLI  
FLVWLILLRRKDKERYEEBERPNEIREDAEAPKARLVKPPSSSSGSRSSGSSSTRSTANS  
ASRSQRTLTDAAPQPLATQAYSILVEPVRGSEPKVKPHANLTKAETTPSMIPQSRAFOT

amino acids 1-16

amino acids 232-251



# FIGURE 25

GTGCTTCCTTTGCTCTCTCGCGCCAGTCTCTCTCTGCTTCTCTCTCAGCCGCTGTTCGGAGGAGACACCCGGA  
 GAGCGGGCTGCAGTCTCGCGCGGCTTCTCTCCCGCTGGGCGGCTCTCGCCGCTGGGACAGGTGCTGAGCGCCCTAG  
 AGCTCCCTTTGCGCGCTCTCTCTCTGCGCGCCGAGCAGTGCACATGGGTTGTGGAGGTAGATGGGCTCTCCG  
 GCCCGGAGCGGCGGTGGATCGGCGCTGGGAGAGCAGCGCGGATTTCAGCTGCCCCGCGCGCCCGGGG  
 CCCCCTGCGAGTCCCGGTTTCAGCCATAGGGGACCTCTCCGAGCAGCAGCACCTCTCGCTCTCTGAGCGGATC  
 GCGCGCGGAGCCACAGCCACGATGATCGCGGCTCCCTTCTCTGCTTGGATTCTTAGCACCCACAGCTCAG  
 CCAGAACAGAGGGCTTCGATCTCATTTGGCCATATACGCCATGTTGACCGTGCACCGCGGCGAGGTCTAACCTGT  
 GACAAGTGTCCAGCAGGAACCTATGCTCTCTGAGCATTTGTAACACACAGCTCTGCGGCTCTGAGCAGTGTGCCCT  
 GTGGGACCTTTACAGGACATGAGAAATGGCATGAGAAATGCCATGCTAGTACGCCATCGCCATGGCCCAATG  
 ATTGAGAAATACCTTGTCTGCTCTGACTGACCGAGAAATGCACTTGCACCTGGCATGTTCCAGTCTTAACGCT  
 CTCTCCATCTTATGTTCCCAAGGACATGAATCCAACTCTTCTGCTCTGTTAGACAAAGGTAATG  
 AGTAGCATCCAGGAAGGGACAGTCCCTGACACACAGCTCAGCAGGGGGAGGAAGACGTGAACAGACCCCT  
 CCAAACTTCAGGTAGTCAACCAACGACAGGCGCCCAACACAGACATCTTGAAGCTGCTCGCGCTCATGGAG  
 GGCATGGGGCGAGAGTTCAGCAGCGCCATCAAGGGCCCCAGAGGGGACATCTTAGACAGAACCTACACAG  
 CATTTTGACATCAATGAGCATTTGCCCTGGATGATTTGCTTTTCTGCTGCTGTGGTCTTGTGGTGTGTTGGTG  
 TGCAGTATCCGGAAGCTTCGAGGACTCTGAAAGGGGCCCCGCGAGGATCCAGTGCCATTTGTGGAAGGCA  
 GGGCTGAAGAAATCCATGACTCCAACAGAACCGGGAGAAATGGATCTACTATGCAATGGCCATGTTATCGAT  
 ATCCTGAAGCTTTAGCAGCCCAAGTGGGAGCCAGTGGAAAGATATCTATCAGTTCTTTGTCAATGGCAGTGA  
 AGGGAGGTTGTGCTTTTCTCAATGGGTACACAGCGACACAGAGCGGGCTACGCGACTCTGCAGCACTGGACC  
 ATCCGGGGCCCCGAGGCCAGCTCGCCAGCTAATTAGCGCCCTGCGCGACACCGGAGAAAGATGTTGTGGAG  
 AAGATTCTGTGGCTGATGGAAAGACACCCAGCTGGAAACTGACAACTAGCTCTCCGATGAGCCCCAGCCCG  
 CTTAGCCGAGCCCCATCCCGAGCCCCAAGCGAACTTGAAGTTCCGCTCTCTGACCGTGGAGCGTTCCCCA  
 CAGGACAAGAACAGGGCTTCTCTGGATGAGTTCGGAGCCCTTCTCGCTGTGACTCTAATCTCAGCGGGCTCC  
 TCCGCGCTGAGCAGGAACGGTTCTTTATTACCAAGAAAGAGGACACAGTGTGCGCGCATGCTCCCTGAGC  
 CCGTGTGACTTCAGCCCTATCTTTGATGACATGCTTCACTTTCTAATCTGAGAGCTCTCGGTTGATTGAAGAG  
 ATTCCCCAGGCTGAGGACAACCTAGACCGGCTATTGCAATATTGAGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
 CTCTGGACTCTGTTTATAGCCATCTCTGACCTGCTGTAGAACATAGGATACCTGATCTGGAATTTACTCA  
 TTATAGTGGCAGGGTGGTTTATTTTCTCTGTTTCTGATTTTGTGTTTGGGTTGTGGTGTGTTGTGTT  
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAAGGATTAAGGCTCTGAGTCTTCTCTCTCTCTCT  
 TCTCTCTCTTTTATTTTAAATTAACCTCTCTGGAAGTTGGTTTATAGGCTTTGCGAGGTGAACCTGTTGGAA  
 ATACCCACCACTAAAGTTTATTTAAGTTCCATATTTTCTCATTTTGCTCTTTATGATTTTCAAGATTATTCG  
 TGCATTTAAATTTACTTAACTTACCAATAAATGAGTGTGACTTTCCACACACTGGATTGTGAGGCTCTTAAC  
 TTTCTTTAATGATATAATGCTGTGATCCTATAGCAGTCTTTATGTCCTTAACATTTCACACCTACTTTT  
 AAAAACAATATTATTAATTTTATTTATTTATTTGTTTGTCTTTATAAATTTCTTAAAGATTAGAAAAATTTAAGA  
 CCCCATTGAGTTACTCTAATGCAATCAACTTTGAGTTATCTTTTAAATATGCTCTGTATAGTTTATATTCATGG  
 CTGAACTTTGACACACTATTGCTGATTGTATGGTTTTCACCTGGACACCGGTGAGAACTCTTGAATTTCTGTAC  
 TCTTTTATGCTAATGCTCTGGGCTGGAGAAATGAATCTCAAGCCATCAGGATTTGCTAATTAAAGTGCTT  
 GACACTGGGCCCCAAGAACTTGAACCTTCACTTTTAGGATTGAGCTGTTTGGAAACACATTGCTGCACTTT  
 GGAAGTCAAAATCAAGTGCAGTGGCGCCCTTTCATAGAGAAATTTGCCAGCTTTGCTTTAAAGATGCTCTG  
 TTTTATTATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCTTGGCTGGGATCTCTTCAACAAAT  
 ACTTTTAAATAAAATGGCTGCAACTGAAGAACCCTTGTCTGATATATTGCAACTGCTCCCATTTTAAAGT  
 TACCTTCTAATGCTCAGTTGCTCCAGGTTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGTTGTGG  
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCCTCAAGTGTACTAATTTATTAATAAAATTAGGTTTGTGTA  
 AAAAAAAA

04975385.101601

## FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNGKGFVDESEPLL  
RCDSTSSGSSALSRRNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEIIGVKSQEASQTL LDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTCCGTGGTGCCATCTACATTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
CATGGGGGAAAAATGATCCGCGTGCTGTTGAAGCCCCCTTCTCAITCCGATCGCTTTTGGCC  
TTGATGATTTGAAAAATAAGTCTGTGTGCACCGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCGGGTGGGTGGTCAGAATGCCGTGCTCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCGTGTGCCAAC  
TGGGTTTCCCAAGCTATGTGAGTTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCGATT  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCCTCTGGCCACGTGGTTACCTTGACGTGCACAGCCT  
GTGGTCATAGAAGGGGCTACAGCTCAGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCAC  
GCCCTCTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAGAGTGTGCTGGACGTCAGGATGGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCCTGTCTGAACCACGCGGCGCTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAG  
TTAGTGGGAGCGACCACTTGTGGCATCGGCTCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTCACTCCTTCTTGAGCTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCTCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCCTTGGAGCTCTGAGTTCGGGCACCA  
GTAGCAGGCCGGAAGAGGCCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTT  
GTTTTTTGTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCTCCGCTTCCCTGGTTCAGCGATTCTCTGCGCTCAGCTTCCCCA  
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAATAATTTTGTATTTTGTAGAGAC  
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCCTGCT  
CAGCTCCCACAGTGTGGGATTACAGGCATGGGCCACCGCCTAGCCTCAGCTCCTTTC  
TGATCTTCACTAAGAAACAAAGAACGAGCAACTTGCAAGGGCGGCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCAGGGTCTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAGC  
TGCAAAGCCCAACAGCCACTCAGAAAAGACGACCCAGCCAGAAAGTGCAGAACTGCAGTC  
ACTGCAGTTTTTCATCTCTAGGGACCAGAACCAAAACCCACCTTTCTACTTCCAAGACTTAT  
TTTTCACTGTGGGAGGTTAATCTAGGAATGACTGTTTAAGGCCTATTTTCATGATTTTCTT  
TGTAGCATTTGGTGTCTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCCCTCCCT  
CAATGTCTGGCGTGTCTGCGTGGAGTGGTGACGTGAATCAAATCATCCACTGAAA

**U.S. DEPARTMENT OF AGRICULTURE**

```
><subunit 1 of 1, 453 aa, 1 stop
```

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIIALILAILAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLBQGQFREEFVSIIDHLLPDDKVLTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQFPWQASLQFGYHLCCGGSVITPLWIIITAAHCYVDLYLEFKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLITFNEMIQPVCALPNSEENFPDGKVCWTSGWGATEDGGDASFVLNHAAPVLISNKCINHRDVTGGIISPSMLCAGLYLTGGVSDSCQDGGGLVLCQERRLKLVLGATSFSGIGCAEVNKPGVYTVTSFLDWIHEOMERDLTKT

amino acids 1-20

## amino acids 240-284

amino acids 240-284

# FIGURE 29

CCCACGCGTCCGTCCTAGTCCCGGGCCAACTCGGACAGTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT  
 GCCAGAAACGGCGCGCGCGCGCACGACGACACACACGGGGGAAACCTTTTTTAAAAATGAAAGGCTAGRAAGA  
 GCTCAGCGCGCGCGCGCGCTGCGCGAGGGCTCGGAGCTGACTGCGCGGAGGACAGGAAATCCTCCGGTGCAGA  
 CGCCCGCGCCGGCTCGCGCGCCCGTGGGATGGTGACGCTCGCCCGCGGGCCCGAGAGCTGTGTCACITGAAG  
 GCGCGGACAGTGGCAGCGCGCGCTGCGCGCTGCTCCCGCGCGCGCCCTCCTGCTCGCCCTGGCGCGTGTCT  
 GCTCGCGCTGCGGAGCGCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
 TCGGATGGGGACCTCTGGATCCCACTGAAGAGCTTCGACTCCAGAATCATCCAGAAGTGTGAATATTCGACT  
 ACAACGGGAAGACAAAGACTGATATAAATCTGGAAGAAATGAGGTCTCATTTCCAGCAGTTTTCACGGAAC  
 CCACTATCTGCAAGACCGGTACTGTATGCTCCTCGCTCGAAATACACGGGTCACTGTTACTACCATGGACATGT  
 ACGGGATATTCTGATTCAAGCAGTCACTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAATATGA  
 AAGCTATGTTCTAGAACCRAATGAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAGCTGAAAGGCT  
 CCGGGATCATGTGGATCAATCACACACCAAACTCGTGCAGAAAGATGTTTCCACCAACCTCTCAGAC  
 ATGGGCAAGAGGACATAAAGAGAGACCTCAAGGCACTAAGTATGTGGAGCTGGTGTCTGCGGACAGAACCG  
 AGAGTTTCAGAGGCAAGGAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGTCTAATCACTGTGACAA  
 GTTTTACAGACCACTGAACATTTCGATTCGTTGGTAGGCGTGGAAAGTGGAAATGACATGGCAAAATGCTCTGT  
 AAGTCAGGACCACTCACCAGCCTCATGAATTTCTGGAGCTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA  
 TGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAAGGCAACCACTCGGCAATGGCCCCAATCATGAGCATGTG  
 CACGCGAGACCACTGCGGGGAATTTGTCATGGACCATTCAGCAATCCCTTGGTGCAGCGCTGACCTGGGCA  
 TGAGCTGGGCCCAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT  
 GGAGACACGCGCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTCGCGGAAGTCAGGGAGTCTTTCCGGGGCCA  
 GAAGTGTGGGAACAGATTTGTGGAAGAAAGGAGGAGTGTGACTGTGGGAGCCAGAGGAATGTATGAATCGCTG  
 CTGCAATGCCACCACTGTACCTGAAGCCGGAAGCTGTGTGCGCACATGGGCTGTGTGTGAAGATGCCAGCT  
 GAAGCTCGCAGGAACAGCGGTGAGGACTCCAGCAACTCTCTGTGACCTCCAGAGTCTCTGACAGGGGCCAGCCC  
 TCACTGCCCCAGCAATGTGTACCTGACGATGGGCATCATGTGAGGATGTGAGCGCTACTGCTCAATGGCAT  
 CTGCCAGACTCACAGCAGCAGTGTGTGACGCTCTGGGACCAAGTGTCTAAACCTGCCCTGGGATCTGCTTTGA  
 GAGAGTCAATTCGAGGTGATCTTATGSCAACTGTGGCAAGTCTCGAAGAGTTCTCTTGGCAATGGAGATCGAGAT  
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCGACCGGCCAGTCACTGTTGCAATGCTGCTTTC  
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTTCTGTCGCGGGGACCAAGTGTACTTTGGCGCATGA  
 CATGCCGGAACCCAGGCGTGTGCTGTGAGGCAAAAGTGTGAGATGGAAGAAATCTGCTGATCTGTCAATGTCA  
 AAATATTAGTGTCTTTGGGGTTCAAGAGTGTGCAATGCACTGCCAGCGCAGAGGGGTGTGCAACACAGGAAGAA  
 CTGCCACTGCGAGGCCCATCTGGGCACTCCCTCTGTGACAAAGTTTGGCTTTGGAGGAAGCAGACAGCGGCCCC  
 CATCCGGAAGGAGGACAGGAGCTGACAGTCCACAGGAGGCGCGCCCTGAGCAGGAGGACCTGGTGG  
 ATGCGCAGGAGCATGCGTCTACTGCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACAGTGT  
 CTGCTCAGAGGAGTCACTGCGTCCCAAGGCTCTGCTGACTGGCAGCATTGACTCTGTGGCTTTGGCATCGTT  
 TCCATGACACAGACACACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCTTACCAGGACGCTGTGAGAAA  
 CAGTGCAGGAGGCGCAGCATCTCTGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGTCTGCTCTGAG  
 AGAGTAGCAGTTTACACTCTGCGAGGCCCGAGCCCTGAGCAGGAGGAAGGAGTCAAAAGTCTGGCCCTTTC  
 ACTGAGCCTCGCAGCAGTGTGGGGAGAAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCAAGTGACACCTCAGCCT  
 TGGCAGCCTGTATGACTGTGCTCTGCGTGCACCTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAT  
 AGCAGGCTTTTAGTTTAAATTTATCAGAGACCTTGCCACCCATCCATCTCCATCCAAGCAACTGAATGGCAA  
 TGAACCAACTGGAGAAAGAGTGAAGAAAGGGCGGTGAACCTCTGGCTCTTTGCTGGACATGCTGACAGCAG  
 AGTACTCAGGTTTGAAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCAACCAACCTTCATTTAAACAGTAGAAGAA  
 TGTAAAGAGTGAACCAATGTAAGAGCCTTAATCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGATTT  
 GAAT

0970505.101601

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624  
><subunit 1 of 1, 735 aa, 1 stop  
><MW: 80177, pI: 7.08, NX(S/T): 5  
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYHGHVVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQROGKDEKVKQRLIEIANHVDKF  
YRPLNIRIVLVGVEVWMDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGI VMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYPPPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRPFVEEGEE  
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGFGAKPAPGICFERVNSAGDPYGN  
CGKVS KSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLQQGGRI LCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRCQONI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGP IRQAEARQEAAESNRERGGQGE PVGSQEHASTASITLI

Signal peptide:

amino acids 1-28

0970557060  
109601.559745

## FIGURE 31

TCCCAAGGCTTCTTGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

097855.101601

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCAACCGTGTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAAACTTTTAAAGAGTTAAT  
GAAACCATACTTTTACATTTTAAATGACAGGAAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTAATATGTAATAA  
TACCAAATATCAATAATACTTATCTCTGGGTA AAAACCTCTTCTCATACCTGTGCTAACAA  
CTTTTAAACAAAAAATTTGCATCACTTTTAAAGATCAAGAAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGGAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCCTACTTGTCTATCTCCCTGCACCGAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT  
CCTTTAACCCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAAAGTGCCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAAGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA



### FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLAL  
LHLVH

Signal peptide:

amino acids 15-27

0978585-301601

# FIGURE 34

GCCGCGGCGAGAGCGCGCCGACCCCGCGCGATGCCGCGCGCCAGGACGCCCTCCTCCGCTGCTGGCCCGGC  
 CGGCGGCCCTGACTTGGCTGCTGCTGCTGCTGCGGCATGGCGGCGGGCGCTGGGCGCCCGCGGCCAGG  
 AGCGCGGCGCGCGCGCGCGCGGCGAGCGGGCCCCCGCGCGGAGAGCGCGGAGGACGAGGACCCCGACAGCAGCACC  
 TGTACACGCGCGACATGTTCAAGCACGGGATCCAGAGCGCGCGCACTTCGTCACTTCTTCGCGCCCTTGGTGTG  
 GACACTGGCCAGCGGCTGACGCGCACTTGGAAATGACTGGGAGACAAATACAACAGCATGGAAAGATGCCAAAGTCT  
 ATGTGGCTAAAGTGGACTGCACGCGCCCACTCCGACGCTGTGCTCCGCCCAGGGGGTGGGAGGATACCCCACTTAA  
 AGCTTTTCAAGCCAGGCGCAAGAGCTGTGAAGTACCAAGGCTCTCGGACTTCCAGACATCGGAAACCTGGATGC  
 TGCAGACACTGAACAGGAGGCGAGTGACACAGAGCGCGGAAGTGGAAACGCCCACTGGCCCCGAGCTCAAGCAAG  
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGACGCTTGCAAGGCGACCACTTTATCAAGTCTTCTGCTC  
 CGTGGTGTGGTCACTGCAAAAGCCCTGGCTCCAACTCGGGAGCAGCTGGCTCTGGGCGCTTGAACATTCCGAAACTG  
 TCAAGATTTGGCAAGGTTGATTTACACAGCACTATGAACCTCTGCTCCGGAACACAGGTTCTGTGGCTATCCCACTC  
 TTCTCTGTTCCGAGATGGGAAAAAGTGGATCAGTACAAGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG  
 TGGAGTCGCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCAACGCCCTCAGAGGCCCGCGTCTGGCAG  
 CTGAGCCCGAGGCTGACAAAGGCACTGTGTGGCACTCACTGAAATAAATTCATGATGACACCAATTCGAGAAGGAA  
 TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCACTTGAAGACTCTGGCTCCTACTTGGGAGGAATCTCTA  
 AAAAGGAATCCCTGCTGCGCGGGGTCAAGATCGCGCAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA  
 AGTATTCGGTACGAGGCTACCCCAAGTTATTGCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCAAGTGGAGGCA  
 GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCGCAAGCGAAAGACGAACCTTTAGGAACAACAGTTGGAGGTCA  
 CTCTCCTGCCAGCTCCCGCACCTGCGTTTAGGAGTCACTCCACAGAGGCCACTGGGTTCCAGATGGTGGCT  
 GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTCTTTGTGTGTGTGTTTCCAAAGCAACACACTCTACAG  
 ATTCTTTAATTAAGTTAAGTTTCTAAGTAAATGTGTAACCTATGGTCACTGTGTAAACATTTTCACTGGCGATA  
 TATCCCTTTGACCTTCTCTGATGAATTTACATGGTTCTCTTGAAGACTAAAATAGCGTTGAGGGAATGAAA  
 TTGCTGGACTATTGTGGCTCCTGAGTTGAGTGATTTGGTGAAAGAAAGCACTTCAAGCATAGTTTATCTGTC  
 CCACGAGTTCTGGAAAGGTGGCCCTTGTGCGAGTATTGACGTTCTCTGATCTTAAAGTCAAGTGTGATCAATAC  
 TGTGTGTGTCGCTAGCATGGACAGATTGAATGCAAAACCCACACTCTGGAAGATACCTTCAAGGCCCTGCG  
 TGGAGCTCTGTGTGTGTAATCTCTCTCAGTGTGAGAGGTAGCCGCTGATGAAGACAGGCTTACTTCTGACC  
 TGTGTGTGTCGCTAGCATGGACAGATTGAATGCAAAACCCACACTCTGGAAGATACCTTCAAGTGTCTGAGGGAT  
 CCTCTGTTTCTCAAGGGGTGAACATGTCTTTAGTTCCCTCATGTAAACAGAACCCAGAGCCCATGAAGTGT  
 TGGATGTCTCTCTTGAAGAGGTAGGCGATGGAAATTCACAGAGCTCTTCTCAGTATCTCATTAATCTATTGA  
 AAGATTCCAGTTGATTTGTCACTGCGGTGACAGACAGACAGGCTTTCCAGGCTCGGATATCCAGGAGGC  
 TCTGACGCGCTGCTGAAGGCGCTTAACAGAGTTCTAGAGTTCTTCTGATTTCTCAGTAGTCTCTTTAGAGG  
 CTGCTTATCTTGGTCTGCTTCAAGAGAGTCAAGCTCTTAATGTATGAAGAAATGGAGTCAATTTGATCTCAAGAC  
 CAAGACAGATGCTGAGTGGCTGCTCTGCGCTGGTGTGACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTTA  
 ACTCATGCTGTCTTGTGATTAACCACTCTATCTCCCTTGGAAATAAGCAATCAAGGCTTAAGCTCTAAGATA  
 GATAGTGTGTTGCTCTTTTACCATCGAGTACTTCCCAATAAACCACCTTTCATCTCAAGACTCTTCAACCCACCT  
 CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGTAGGAATCTTAGAAACAAAGACCACTTATA  
 CTGCTCTGTGAGGCGAAGATAACAGCAGCATCTGACACAGCTCTGCTCTAAAGGAAATCTTTATTAAATCAG  
 TATGGTTACAGATAATCTTTTAAAAAAACCAACCTCTAGAGAAGCAACCTGTCAAGAGTCTTGTACA  
 CACAACCTCAGCTTGCATCAGAGTCTTGATATCCAGAAATCAAGTGGTACAATTTGTTTGTATCACTAT  
 GATACCTTCTAAATAAATCTTTTATTTTAA

007055 104501

## **FIGURE 35**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776  
><subunit 1 of 1, 432 aa, 1 stop  
><MW: 47629, pI: 5.90, NX(S/T): 0  
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLTYADMFTTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWMQLTLINEEPVTPEPEVEPPSAPE  
LKQGLYELASANFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHVELCSGNQVRGYPTLLWFRDGGKVDQYKGRDLESLEYYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

0070505 107001  
107001 5050260

CTTTTCTGAGGAACCCAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTCACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATAATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAAGGATTTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTTGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCTGTGACCGTCAATTACAGTTATTGTTATCCATCCTTTTTTTCTGTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAAACTGAGGTATGGAGCCT  
CCATGATCAAAAAAATAAAAAA

BOOKS RECEIVED

><subunit 1 of 1, 277 aa, 1 stop

MNGFASLLRRNQFILVLVFLQLIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEGKDPGEEG  
KHGKVGVRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPEGKKGAGTVCDGRY  
RKFGVQLDISIARLKTSMKFVNVIAGIRETEEKFFYIVQEEKNYRESLTHCRIRGGMILAMP  
KDEANITLIADYVAKSGFFRVFIVGNDLEREGQYMSDNTPLQNYSNWNEGEPSPDPYGHEDC  
VEMLSRGRWNDTECHLTMYVFCEFIKKKK

Signal peptide:

amino acids 1-25

## FIGURE 38

GGTTCTATCGATTGGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCCGTGTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
CCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTACGTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCAGCGCGCTGGAACAGACCGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCTGTCTGTGTGTACCGTGTCTGTCTGA  
AGCTACACCTCTGGCCCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCTGGCCGCGGCTGCCGCCGACCCGGAAG  
TCCCGAGGGGGCTGACGCTGGCTGGCGCCTCGCGGAACCTGGCCAGCAGCGCGCGCGC  
ACACCTTTCTCATTCACGGCTCGCGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGTAAC  
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGCGACAG  
CGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGAGATGCACGCGCG  
GAAGCGCGCGGAGTTTGC CGGAGGGGACGCTGCGCCAGAGGTGGAGGAGCGCGCGCCCT  
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGTGGCTCTG  
GTTGGGCTGGCCAGGCGCGCTGCGCACTGCTTTGTGCCCCACCGCCTGCGCCGGGGCC  
CCCTGTCTGCACTGCTCCGCACTGCGCGCGCGCGCGCTGGTGTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGAGCTGCCGCCCTGAGAGCCATGGGGCTCCACTGTGGCTGCGAG  
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCGTACATCTTC  
ACCTCTGGCACCGCGGCCCTCCCAAGGCTGCTCGGATCAGTCACTGAAGCTCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACAGGAAGATGTATCTACCTCGCCCTCCAC  
TCTACCATGTTCGGTTTCCCTGCTGGGCATCGTGGGCTGCACTGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTCCGATACCTTGTCAACAGCCCGGAGCAGGCGAG  
AACCTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGAGCGCT  
TTTGTGCGGCGCTTCCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACAGGACAGCGGGGCGCTGTGGGGCGTGTCTTCTGGCTTTTACAAGC  
ATATCTTCCCTTCTCCTTGATTGCTATGATGTACCCAGGAGAGCCAAATTCGGGACCCC  
CAGGGGCATGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAAGCA  
GCAGTCCCATCTTCTGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCTGGGAGTGTCTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACCTTGCCACCTTATGCCCC  
GCCCCGATTTCTCAGGCTCCAGGAGTCTTTGGCCACACAGAGACCTTCAAGACAGCAAGAA  
TTCGATGGCAAAATGAGGGCTTCGACCCCGACACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCTTACCTGCCCTCACAACTGCGCGGTCAGCCCTCTGCGCAGGAAA  
CCTTCGAATCTGAGAACCTTCCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGTGGGG  
CCGTGTCAGGTGTACTGGGCTGTGAGGATCTTTCTATACAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGACCTTAAAAAATAAAAAAATAA  
AAAAAAGGGCGCGCGGACTCTAGAGTCGACCTGCGAGTAGGATAACAGGGTAATAAGC  
TTGGCCGCATGGCCCAACTTGTTATTGACG

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFFSYSEAESNRARAFLRALGWDWGPDPGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGVPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFYIIGELCRYLVNQPP  
SKAERGHKVRVLAVGSGRLRPTDWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVVSQQSPFLGYAGGPELAQQK  
LLKDVFRPGDVFVNTGDLVLCDDQGFLRFHRTGDTFRWKGENVATTEVAEVEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYPARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLR

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486

00976505.101501

## FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACAC  
CACATCCCCAAGAACTCTGAGCTCACACCAACAGACACACGCGGCATACACACTCGCTCTC  
GCTTGTCATCTCCCTCCGGGGAGCCGGCGCGCTCCACCTTTGGCGCACATCCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTTGCGGGCTCGGAATCGGATTTGCAGCTCTGAAACCC  
CCATGGTGGTTTTTAAACACTTCTTTCTCTCTCTCTCGTTTGAATTGCACCGTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGGCTTGCCATCGT  
CCATCTGGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCTCGG  
CTGGCAGAAAGGGGTGACGCTGGGCAGCGGCAGGAGCGCGCCCTGCTCTGGGCGGGCTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGCCGTGGGGTTTACCGAGCTGGATTGTATG  
TTGCACCATGCTCTTTGGATCGGGGCTGTGATTCTTCCCTCTTTGGGGCTGCTGCTCTCCC  
TCCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTTCCCGCAGGCGTACGGTGCC  
AAGGGATTGAGCCTGGCGGACATCCCCCTACAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCAAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAC  
TCGAATTTGAAAACCTTTGTGGAAGAGACAAGCCATTTTGTGCGCACCTTTTGTGTCCAGG  
CATAAGAAATTTGACCAATTTTCCGAGAGCTCCTGGAGAATGAGAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGCGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCTCGAACCGGATGTTTACGCTGATAAACCTTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTAGCAATACTGACAGCTCAAGCCATTGGAGACGTGCCCC  
GGAAACTGAAGATTGAGGTTACCCGCGCTTCATTGCTGCCAGGACCTTGTCTCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTGAGCCCAACCCAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCATACTGTGCGGGGCTTCCACTGTGAGGCCCTGCA  
ACAACTACTGCTCTCAACGTCATGAAGGGCTGCTTGGCAATCAGGCTGACCTCGACACAGAG  
TGGAACTCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGCATGGAGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAAGGTGTCTGCAAGGTCTTTCAGGGATGTGGTCAGCCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACAGTTTCAGGCCCTACAATCCTGA  
GGAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGCTCAGACAGATAAAAGAGA  
AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCTTCACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATCTT  
GCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCGTGACACTTTTATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAACCGCTCAACAATGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAAGTTTGTGCCA  
CAGAGGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCGAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGCGCATGCGAGACTGTGCGAGATA  
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTGTTTTCCAAAGAGTACCGGGTGCCAGACTGAACTG  
CTTCTCTCTTCTCAGCTATCTGTGGGACCTTGTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTCTGACAGGAGATTTTCTTACCTTCAATTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCAGTGTGAGGGTTTTTTTTTCTCATTAAAAAT

097555 101601



## **FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAESLSLNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFOLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPTYICKDESVTAGTSNEEECWNGHSKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDDVCPTFEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

1097535 104601

# FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCA CG  
CAGTTTTCGACGCGCTTCGCGCGGGTGCGCCAACTACGCAAAAGACCAAGCGGGCTCCGCGCGGACCGGCGCGGGG  
TAGGGACCCGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTCGCGAGGT  
GGAGGGAGATCAGGAAAACGGCTTCTTCCTCACTTCGCGCGCTGGTGAGTGTTCGGGGAGATTGGCAAAACGCTTAGG  
AAAGGACTCGGGGAAAATAGCCCTGGGAAAAGTGGAGAAGGTGATCAGGAGGCGGGTCCACTACGCGAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCTCCACTTCGAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCTCGCGCGCTCCGTACCGCACTCCAGGAGAGTCAGCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA  
AAAGTCTCTGTCACCTGTATCTCAATTCTGCTGGTTTTTTTCTCCGAAAGATTGGTGAGAACTGGAATGTGC  
ACTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTTCTTCGAGTCCCATTCATTAAAGCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGTTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGATCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCGCGAGCGCGCGGGCGCGTGGTTCTCGCGTGGAGTCTCACTGGGACCTGAGTGAATGCTCCCA  
GGGCTGTGCGGGGCATCGCCTTCGCGCTTCTCCACAGGCTGTGTCTGTCTGCGAAAGATTGGCAAACTGGGGG  
CGCTGGCAGGATTCTGATCCTCTGCTCTCACTTATGGTTACCTGTCTGGGGCCAGGCGCTTAGAAGAGGAGG  
AAGAAGGGCGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACTTCCACCTCCAGCGCCATCTCA  
TTTTCTCTAGCGGATGATCAGGATTTAGAGATGTGGTTTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGCTCGCGAAGGAGTTAACTGGAGAATACTATGTCCAGCTATTGCAACCATCCAGGAGTCAGT  
TTATTACTGGAAGTATCAGATACACCGGACTTCAACATTCTATCATAGACCTACCCACCCACTGTTTATC  
CTCTGACAATGCCACCTACCTCAGAACTGAAGGAGGTGGATAITCAACGCATATGGTCGGAAAATGGCACT  
TGGGTTTTAACAGAAAAGAAATGCATGCCACAGAGAGGATTGATACCTTTTTTGGTCCCTTTTGGGAAGTG  
GGGATTACTATACACTGTCAAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAAATGGCATATATCCACAGATGTACTCAGAGAGTACAGCAAACTTATGCTTCCATA  
ACCCCAACAAAGCCTATATTTTATATATGCTATCAAGCTGTTCTATTCACCACTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAAACACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGATTAACGTGCCCTCAGAGGTAGCAAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCATG  
ACTGTTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCACTAGATGGCTATGATATCT  
GGGAGACCATAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCCTGGGCAAGAGGACTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG  
GTGGCAACATGAACGGATCACTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCAGACCGGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGGAGGCTCTCAAGTTCAACAAAAC  
TGCAGTGCCCGTCAGGTATCCCCCAAAGACCCAGAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAGAAAGCCAAAGCAAAATCAGGCTGAGAAAAGCAAAAGAAAAGCAAAAGAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACTGGCCGCCCACTGAAAACCTGTCTGCTCAGTG  
CCAAGGTGCTACTCTTGCAGGCCACACTTAGAGAGAGTGGAGATGTTATTCTCTCGCTCCTTTAGAAAACGCTG  
GTGAGTCTCAGTTCCTGCTGCTGCTTCACTGACCTGACCAACACTGCTTTGAATATAGGAGGAGAAACAATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAGACTACCTTTGATAAATTAC

## 099755-10501

[illegible]

## 0976953 in 11501

```
><subunit 1 of 1, 515 aa, 1 stop
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MAPRCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAAGVKLENNYVQPICTP  
SRSQFITGKYQHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFNRKEC  
MPTRRGFDTFFGSLGSGDYTHYKCDSPGMCGYLDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCCLDEAINNVTLA  
LKYTGfYNNsIIiYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCK  
ELVHITDWTYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QOAMSGTWLQSSQSECESTGNCLQEILATATGSPLSLSATWDRGTGTMNGSPCQLAKVYGS  
TSQPTHMRGWTYLTGIGIES

**Signal Peptide:**

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

# FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCTCTGCCCCGGAGCCTTGCCTCCCGCTCCTGCTCTCTCTGGGTGGCAG  
GTGGTTTCGGGAAACGCGGCCAGTGCAAGGCATCACGGGTGTGTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCTACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAACAAAT  
GCAGATGCTTTCCAGGATACACCGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGCCATGCCAACACAGATGTGTGAATACACACGGGAAGCTCAAGTGTCTTTGCCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA  
ACTGTCACTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTCA  
TTGGTTTCSAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGACGCCACCATGCCAATTGCTTCAATACCCAGGGGTCTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCTGAAAATCTCTG  
TGAAGGAAGTCTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTGTCTCAC  
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAATAATGTTACCCAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACCTTGCGAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAAATGAAGAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT  
AAGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAGCGCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAACATTTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTGGGAAACCTTCGAGTGTGTGAAAAACAGTAAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAACCTGATGC  
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCAGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTCTTTCAGGCTTATGTCCAGATAGCCTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTGACTTTGTATGTGCTAGTTCCCTGGTTTTTTTGATATTGCATCATAG  
GACCTCTGGCATTCTTAGAATTACTAGCTGAAAAATTTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATAGAATATGCCAATATTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTCTGAATCTTTCCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTACACATTTCTA  
GAAAATAGAAAAAAGCACAGAGAAATGTTAACTGTTTGTACTCTTATGATACTTCTTGGA  
AATCATGACATCAAAGATAGACTTTTGCTTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTAAATCTTTGTAATAATAA

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC

UNIVERSITY OF CALIFORNIA

Signal peptide:

EGF-like domain cysteine pattern signature.

### Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

## FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCTGAGGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC  
AGAATGGGAGCTGACTGATATGGTGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAGAAGATGCCTAGAGAATGGCAATTTAAAGAAAAAGATATACT  
TGTTTTGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAATACTTAGGGACGGTGTCT  
CTTGACAAAATGTGTTCTGCCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTAAGACAAAACTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTGCTTCCAACATGGAATGAAATAAAAATAAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

007525.01601  
10901059266

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVVVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQKIKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGLIIVSNICPGP  
VQSNIVENSLAGEVTTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLIVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

09/05/10 10:50:10



# FIGURE 48

GCACGCTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTGGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCGGACAGCGCTGGGCCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCGTGAT  
GTGGCTCAGTTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCTGTGGCAGACAC  
CTGGGTCTCCTGCTGCTGCCACTGCTTTGAAAGGCGAGCAGCAACAGAACTGAAATTCCTGGT  
CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGTG  
GCTGCCCTGCGAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCGAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAAGTGTCTCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTGCCTCCACATGTAACGTATACAAACAGCT  
GCACAGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGCCCCAGCCTG  
GGGTGCAGGGCCCTGTGTCAGGAGATTCCGGGGCCCTGTGCTGTGCTCGAGCCTGACGGA  
CACTGGGTTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCGAGGCTCGAGTTTCAGGGGGCAGCTT  
TCCTGGCCAGAGCCAGAGACCCCGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCCAGGACAGCTGGCCTGTGGCGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCTGCATGGAGCCTACACCCACCTGAGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCCC  
TCTGCCTGCCCTATCTGACCCACACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCCGTGACCTCTGGGGCCTAG  
GGCCTGCGAGCCGCTGCATGCAGCTCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCACTGCTGTGGGTGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGT  
CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAAG  
CCCCGCCAGGCCGCGGCTTTACCCGCGCTCCCTGCCTATGAGGACTGGGTGAGAGTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACGAGAGCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAAATGGCATTACTGCCCTGTCTCCCCACCTGTGATGTGTGATTCCAGGCAC  
CAGGCGAGGCCCAGAGCCACAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA  
CTCCCCACCTCGAGGACAGGGGTGTCTGTGGACACTCCCAACCCAACTGTGCTACCAAGC  
AGGCGTCTCAGTTTTCTCTCTCTTACTCTTTTACAGTACAACTACGCCAGCCAGCTTGT  
TGAAATTTCTTTTTTTGGGGGCAGCAGTTTCTCTTTTTTAAACTTAAATAAATTTGTAC  
AAATAAAA

9979555.101601

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWFWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLNRLRLISRPTCNCIYNQLHQRHLSNPAPRPGMLCGGEPQPGVQGPCQGDSSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQS PETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG  
WVLGRARPGAGISSLQTVPTLLGPRACSRLLHAAPGGDGSPI LPGMVCTSAVGELPSC EGLS  
GAPLVHEVRGTWFLAGLHSPGDACQGPAPPAVF TALPAYEDWVSSLDWQVYFAEEPEPEAE P  
GSCANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

## FIGURE 50

CGGGCCGCCCCGGCCCCCATTGCGGCGGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCAGAGTGGCGCGGGCGGCGAGGGGAGCCTTCCACCACGGGGAG  
CCCAGCTGTGAGCCGCTCACAGGAAGATGCTGCGTGGCGGGGACGCCCTGGCATGGGTGT  
GCATGTGGGTGAGCCCTGGGAGCACTGTGTTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCTCTCC  
CCTGAGCCTGGCTTCACTGCGACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCTATGCCAACCGCACGGGCC  
TCTTCCCGGACCTGTGCGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCG  
GACGAGGGCAGCTTCACTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCT  
GCAGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCAGTGCAGATGGCCAAACGA  
GCAGGGCTGTGTTTGTGTGACAGCGTCCCTGCGGGTGGTGTCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCACAAACCCGTGTGACAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGTATACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGTCTGTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACTGTGAGCCTTATTTCTCCAATGGACATGATTCCAAAGTCATCCTGTGCCTTTT  
TTCTTATAGACACAATGAACAGACACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCTTGTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAAGCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCAGCCCTCAACATCTCTGGAGTCTAGAAGCTGTTTCTTTTC  
CCCTCCTTCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCAACCCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCTATCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTGTGTAACCTGGGGGTATATTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA

007555.10454

## **FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPGPGFSLAQ  
LNLIWQLTDTKQLVHSPAEQGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSLQGYPEAEVFWQDQGGVPL  
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEGSKTALQPLKHSDSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

030750512509460  
109101.2059460

## FIGURE 52

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCCTCTAAGAAGGGGGAGTC  
CTGAACCTTGCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACCGGCTTGAATCTGTTCGTCACCTCTTTGATTTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAAAGCTCATCTTCCCTCTGCTG  
TCTGGGCTATGAAAAAGAAGGAAAAGGTAATAATCCCCAGAAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTGCAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTCAAGAGAGGGCGAGTCATCTTTAA  
AGAACATTTTATTTTATACAAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTTTT  
CTGACTCCTATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTGTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAG  
GCTGAGCGCGCGGATCACTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGCGTGGTGATGCGTGCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCGAGGTTGCGGTAAAGCCGAG  
ATCACCTNACGCTGGACACTCTGTCTCGAAAAAGAAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACTTAGACTTAAGCTGATGAAGCTTGGGCTCCTAGTGT  
TGTTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCTGTTTCTTAAATGGGTAGTCTATAGTATATTATACTACATAACA  
TTGTATCATAAGATAAAGTAGTAAACCACTACATTTTCCCATTTCTGTCTCATCAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTTGTCTCTA  
CTAAAAATCAAAAAATTAGCCAGGCGTGGTGGTGACACCTGTGATCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGAGGTTGCACTGAGCCAGATTTGTGCC  
ACTGCATCCAGCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG  
CCTACAGCAGCTACTATTGAATAAATACCTATCTGAGATT

00075551-00000000

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 24172, pI: 5.99, NX(S/T): 1  
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS  
FHSTHKHNNQPIWFTLGILEALKGWDQGLKGMVCVEKRKLIIIPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDEKDKGFISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

1097855.104501

## FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTAGCAT  
CCAACCATTCCTCCCTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC  
CTGCCACCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCTGCACTTCAACTCTCTGC  
TACACAGTGAACCACAAAAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAAGTCTC  
TGAGGAGATGTTCTCCTCAGTTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACGTCTACATCATGAACCCCTGACGCCCAACCGTGG  
CCATGGCAAGATCCATCTGCGAGTCTCATGGAAGAGCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCCTCCGTGCGGGCTTCTCGCTGTGGTTCATCTTGGTGTGATGGTG  
GTCAGTGTGTGAGGAGAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGATGATGGCGCCAAGTAGTGGGTGGCGGGC  
CTGCGACCTCCCGTGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGTCTCG  
CTCTTGGTGTGCTTCCCGTACCTAGGACCCAGGGCCCACTGGGGCCTCCTGAACCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCACTCTCTTCCATCCGAGAACTTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCGCTGTCACTTCCCCAGTGTCTTGGCTGGCAGTGGCTTACAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTCTGTGTGTGACAGCGTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTCTGA  
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG  
CTGCAGGCAAGCTGGACATGTGCCCTGGGCCAGGAGGGCATGTTGGGCCCTCGTTTCCATT  
GCTAGTGGCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGTTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACTCGCTGGGCAGGGGCAGCCAAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTGGGGCTTCACTGAGAATCTCCAGTT  
GCCCTTGGTGGGGTTTCCACTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG  
GCATAAGGGGAGGCCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTCTGTGGGACAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGGAATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCATCTCTACTAAAATAACAAGATTAGCTGGGCGTG  
GTGGCGTGTGCTGTAATCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAAGCAGAGGTTGCACTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAA

0978585.101501

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415  
<subunit 1 of 1, 215 aa, 1 stop  
<MW: 24326, pI: 6.32, NX(S/T): 4  
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPDRHRGHGKIHLQVLMEEPPEPDSTVAIVIGASVGGFLAVVILVLMVVKCVRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77



## 0697-880X(200306)23:3;1-D

GTGTGATATATGCTCTGAAGTACATCCGTGCATTTTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTTCCACAGTACCTGNCCACCCCTCAACGTCC  
TCAATGGCTCTGACGCCCCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCAACAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG  
TCTCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTCGGGTGATGCTGAGAAAAGTGCAGCCGAGGAGTGGAGGGA  
TTTACAAGTCTACATCATGAACCCCCC

## **FIGURE 57**

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCCTCAACGTCTCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTAACTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTACAAC TGCTACATCATGAACCCCC

0007333-100001

## FIGURE 58

TGCGGCGACCGTCGTACACCATGGGCGCTCCACCTCGGCCCTACCGTGTGGGGCTGCTCCCGGATGGCGCTCCTGT  
TCCTCTTGTGCTGTGAATCTGCTCGCGGACCCAGCGCTCCCGGCCGAGCTCAACCCCGACGTGCTGTGGTCC  
CTGGTGAATTTGGGTAAACCACTGAAGGCCAAGCTGGACAGCCGACGTGGTGCATCTACTCTGCTCCAGAAGA  
CGAAGACTCTTACAACTCTGGCTGAACCTGGAACTGCTGCTGCCTGTCACTATTGACTGTGCTGGATTGACAATA  
TCAGGCTGGTTTACAACAAAACATCCAGGSCACCCAGTTTCCTGTAGTGTGGATGTACGTGTCCCTGCGCTTGT  
GGAAGACCTTCTCCTGGAGTTCCTGGACCCCGAGCAAAAGCAGCGTGGGTTCCTATTTCACACCATGTGGAGA  
GCCTTGTGGCTGGGGCTACACACGGGGTGGAGTATCGAGGGGCTCCCTATGACTGGCGCGAGCCCAAAATG  
AAAACGGGCCCTACTTCTTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCGCTGGTGC  
TGGTTGCCACAGTATGGGCAACATGTACAGCTCTACTTTCTGCAGCGGCAGCCGAGGCTGGGAAGGACAAGT  
ATATCCGGGCTTCTGTCACTGGGTGCGCCCTGGGGGGCGTGGCCAGACCTTGGCGTCTCTGGCTCAGGAG  
ACAACAACCGGATCCAGTATCGGGCCCTGAAAGATCCGGGAGCAGCAGCGGTGACGTGTCTCCACCACTGGC  
TGCTGCCCTACAACATACATGGTCACTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACATCAGCGGG  
ACTACCCGAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCGAGTGCATGCCCTCTATGGTACTGGCGTCCCCACACAGACTCCTTCTACT  
ATGAGAGCTTCCCTGACCGTGACCCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCC  
TGCACTGCCAGGCGCTGGCAGAGCCGCGAGGAGCACCAAGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCATCG  
AGATGCTGGCCAACGCCACCCCTGGCTATCTGAAACGTGTGCTCCTTGGGGCTGTA

CTCCTGTGGCTCGGCGGTGGACCTGTCTGTGGCTCTGGGGCTGTCACTGGCCACCGCTTTTGCAAGGTTTGTA  
CTCACCATTCAAGGCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATTCTCTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGACACTGGATGGCAAGAATGTGCTGATGGTGA  
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCTTGGTCCAGTCCCTGCTGGGGCCATG  
TGTCCCTTATTCTGTGGGCTTTTCACTACTTCTTCTGGGCCCTGGCCCCGACGCTTCTATGAGGGATGTT  
ACTGGGCTGTGGTCTGTGACCCAGAGGTCCAGGGATCGGCTCTGGCCCCCTGGGGTGAACCTTCCACACACCA  
GCCACAGTAGGCTCTGCACTGGTTCATGGGTAGTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCTTGGGCGAGCTTAGTAGCTCTGCAGGAGGGGAGTTTGTGTGGTTCCTTCTGGTTTCCAGGC  
CTTGGGACATCTCACTTCACTTCTACTCTCTTACCACAGGAGCATTAAGCTCTGGATTGGGCAGCAGATGTG  
CCCCAGCTCCCGAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTCAOCTGGGACTGTGGTTCAGAGATGAGAGCAGGGTGGAGCCATGGCTTCTGGGAACCTATGGA  
GAAAGGGAATCCAGAGAGCAGCCAGGCTGCTCGCAGCTTCCCTGAGCTGCACTCTTGTCAACCCACCATCA  
CACTGCCACCTGCCCTAGGCTCTCACTAGTACCAAGTGGGTGAGCAGAGGCTGAGGATGGGGCTCTCTATCCAC  
CTTGGCCAGACCCAGCTTAGTGCTGGGACTAGCCAGAAATCTGAATGGGACCTGAGAGAGCCAGGGGTCCCC  
TGAGGCCCTCCCTAGGCTTCTTCTGTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCTGAGAGT  
CAGGCTGCTTCTCAGCGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCTCTAGGT  
GGGTTCACCAAGAGCGCTTCAAGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCACTGGATTTCCTGT  
TTGCATACATGCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAGTACTCTGGATGCTGTAAAAAAGGAAAAAAAAA

00705570101

087-963-7333

### Important features:

amino acids 1-28

amino acids 147-164

amino acids 99-102, 273-276, 289-292 and 398-401

amino acids 189-201

amino acids 353-365

## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGGCGGCAGCGCGGCGGACGCGGACATGGAGAGCGGG  
GCCTACGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCTGACGCGAGCCGA  
GGTGGTGGCGCGCGCGTGTGCTTGGTCTTCGCCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCGGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCTGCGCTCGGCCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGTCTCTGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTACCAAC  
CAGTGGGCGAGTCACCAACCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCCTTACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCATCAGCCTCCTGGAACTGCCA  
GCCCTCTCTTTCACCTGTTCATCCTGTGTCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGCGTGGCAGAGCCACACCCCAAGTGCTGTGCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCGGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACCAGGCTCTGTGTCTCTCA  
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGCCACCACCTGTGCCGCT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTATGGCACTTCTCTCTG  
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGATTATATAAAATCGTGGGGGAGATGCCCGCCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTTCAAAG

0 5 3 7 3 5 5 1 0 5 5 0 1

## **FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304  
<subunit 1 of 1, 224 aa, 1 stop  
<MW: 24810, pI: 4.75, NX(S/T): 1  
MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDLFLSALWTFWLVFGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

09072503E 101500

# FIGURE 62

GAGCACCCTACCTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
 CCCTGGCCGAGGCCCCCAAGCTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAACGGAGCCAGAGGGG  
 ATGTTCAAGGCCCTGTGAGGACTCCAAGAGAAAAGCCCGGGCTACTCCGCTGGTGGCCCTGTTTGTGCTGCTG  
 GCCCTGCTGGTCTGGCTTCGGCGGGGTGCTACTCTGTTATTTCTAGGGTACAAGCCGAGGTGATGGTCAGC  
 CAGGTGTACTCAGGCACTCTGCGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCGGGGAATCTGATGCCC  
 TTCCGCACTGAAACCGCAAAGCCAGAAGATGCTCAGGAGCTCATCACCAGCACCCGCGCTGGGAACCTTACTAC  
 AACTCAGCTCCGCTATTTCTTTGGGAGGGACCCCTACCTGCTTCTTCTGGTTCATTCTCCAAATCCCGAG  
 CACCGCCGCTGTGCTGAGCCCGAGGTGGTGCAGGCCTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
 TCGCTGCCGCTCCCTACAGGCCCGAGTACGAAGTGGACCCCGAGGGCTTAGTGATCTCTGGAAGCCAGTGTGAAA  
 GACATAGCTGCATTGAATTCACGCTGGGTGTTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCTCCGCTG  
 AAGGGCCCTGACCACTTCGGCTCCAGCTGCTGTTGGCACTGCAAGGCCCCCAAGGACCTCATGCTCAAACTCCGG  
 CTGGAGTGGACGCTGGCAGAGTGGCCGAGCCGACTGGCCATGTATGACGTGGCCGGGGCCCTGGAGAAAGAGGCTC  
 ATCACCTCGGTGTACGGCTGCAGCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGCTGGGGGCCATCATGGGGCTC  
 GTCTGGAAGAGGGCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCGTG  
 GAAGTGAACTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCGAGCTACTAC  
 TCGCCCAAAACCACTGCTCCTGGCACCCTCAGGTCGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC  
 TATGCACTGAGGAGGCAGAAATGATTTGCGGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT  
 GGCTTGGCATCCTCTCAGCCCTACGCCGAGAGGATCCCGTGGTGGCCACGGCCGGGATCAACATCAACTTCAC  
 TCCAGATCTCCCTCACCGGGCCGGGTGTGCGGTGCACTATGGCTTGTACAACCAAGCTCGGACCCCTGCCCTGGA  
 GAGTTCTCTGTTCTGTGAATGGACTCTGTGCTCTGCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT  
 GAGAGAACTCGGTTTGAGAGCCACATTCAGTGCAGAGGAGCAGACATGCATCTCAGTGCCTCAAGGCTCTGT  
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCAGGAAAGGGGTCCCATGTGGGACATTCACC  
 TTTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGTCAGGAGCGC  
 TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCGCATTTGTTGGTGGAGCTGTGTCTCTCCAG  
 GGTGATGGCCATGGCAGGCCAGCTCCAGGTTTCGGGTGCACACATCTGTGGGGCGGCCGACTGTCAGGAGCGC  
 TGGGTGATACAGCTGCCCACTGCTCCAGGAGGACAGCATGGCCTCCAGCGTGTCTGTGACCGTGTCTCTGGG  
 AAGGTGTGGCAGAACTCGCGCTGGCTGGAGAGGTGCTCTCAAGGTGAGCCGCTGCTCTCCGCTACCGTACC  
 GAAGAGGACGACCATGACTACGAGCTGGCGCTGTGTCAGCTCGACACCCGCTGGTGGTGGCTCGGCCGCGCTG  
 CCGCTGTGCTGCCCGCGCTCTCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGTCTGGGGCGCCTTG  
 CGCGAGGGCGGCCCTACGACACGCTCTGCAGAAAGTGGATGTGACTGTATTCACACAGGACTGTGTCAGCGAG  
 GCCATTCTCGTACCAAGTGTGCGCACGATGCTGTGTCGGCTACCGCAAGGCTGGTGGAGTGGCTGTGTCAGG  
 GACTCAGGTGTGCTGGTGTGTCAGGCACTCAGTGGCCGCTGCTTCTGGCGGGCTGGTGGAGTGGGGCCTG  
 GACTGTGGCGGCTCAACTACTTTCGGGCTTACACCCGCTACAGGTCATCAGGTTGATCAGCTGGATCCAGCAAGTGGT  
 ACCTGAAGGAACTGCCCCCTGCAAGCAGGCCCCACCTCTCTGGACTCAGAGAGCCAGGGCAACTGCCCAAGCAGG  
 GGGACAGTATTTCTGGCGGGGTGGGAGAGCAGGCCCTGTGTTGGCAGGAGGTGGCATCTTGTCTGCTGCT  
 CTAGTGTCTGCTCCAGTGTGCGCAGAGGATGGAGAAGTCCAGCAGCTGGGGGTCAAGAAGTCCCTGAGGACC  
 CAGGCCACACAGCAGCCCTTTCGCTCCCAATTTCTCTCTCTCGTCCCTCTCTCACTGCTGCTCAATGAAG  
 CGATGGCTCAGCAGCAGAAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCAATGTACAGAGG  
 CTGTTTGGAGCCTCTGCTCCAGAGGAGGATTCAGCTTCGGAAGCCCTGGTCTAATCTGGATCTGGGAAT  
 GGAAGTGTCTCCATCGGAGGGACCTCAGAGCCCTGGAGACTGCGAGGTGGGCTGCTGCGACTGTAAAGCCAA  
 AAGGTGGGAGTCTGACTCCAGGGTCTTGGCCACCCCTGCTGCCACTCTGGGCGCTCAGCAGCCAGCCCT  
 CACTGGGAGGTGAGCTCAGCTGCCCTTGGAAATAAGCTGCTGATCAAAAAAAAAAAAAAAAAAAAAA

00070505.101601

## FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQMLKELITSTRLGT  
YNNSSSVSYFGEGLPTCFFWFILQIPEHRRMLSPPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLHASSCLWHLQGPDKLML  
KLRLFWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSSTPYFSPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGGEFLCSVNLGCVACDGVKDCPNGLDERNCVCRAFQCKEDSTCIS  
LPKVCDDGQPDCLNGSDEEQCEGVPCGTFTFQCEDRSCVKKPNPQCDGRPCDRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIAADRWVITAACHCFQEDSMASVT  
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCRPNYFGVYTRITGVISWIQQVVT

### Important features:

#### Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

#### N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### Kringle domains.

amino acids 746-758 and 592-609

#### Homologous region to Kallikrein Light Chain:

amino acids 568-779

#### Homologous region to Low-density lipoprotein receptor:

amino acids 451-567



## FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGAT  
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACAGTCGGACCCCCTGCC  
CTGGAGAGTTCTCTGTTCGTGAATGGA CTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGTGTGTCAGCTCGACCAACCGGTGGTGCCTCGGCCCGCTGCGCCC  
CGTCTGCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCTGTGAGGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCACTGGGCGCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCAGAGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAAGTCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGG  
AAGTCCAAGCAGGGGGACAAGTAT

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## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCCTCCAGTCCCCCAGCCCTTGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAACACCAAGAGGTGGTTTTTGTTTTTTAAA  
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCCGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAAACCTTTTTTCATCATTCACGGAT  
GGACGATGAGCGGTATCTTTGAAAACTGGCTGCACAAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCTCTCGGCTTGAGCATTTGGTATTGAGTGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCAC  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCTAGCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCTAGGAAAGGGAATCTTT  
ACAAAAATAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

007855 101601

## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646  
><subunit 1 of 1, 354 aa, 1 stop  
><MW: 39362, pI: 8.35, NX(S/T): 2  
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDVNNTRVVGHISIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT  
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

# FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCGTGGGCAAGGGCCGGGGCGCCGGGCCGAGCCACCTCTTCCCTCCCCCGC  
 TTCCCTGCGCGCTCCGCTGGCTGGAGCGCGCTGGAGGAGTGGAGCAGCACCCCGCGCGCCCTGGGGGGCTGACAGT  
 CGGCAAGATTTTGGCCCGAAGAGGAAGTGGCTCAAACCCCGCCAGCTGGCGACAGAGGCGAGACCAGGGGGCGCTCG  
 CTGCGCTCGGGCGGGCTGTAGGCGAGGGCGCGCCCGCAGTGCCGAGACCAGGGGGCTTTCAGGAGCCGGCCCCGGGAG  
 AGAAGAGTGGCGGGCGGACGAGAGAAACAATCCAAAGTTGGCGAAAGGACCGCGCCCTACTCCCGGGCTGGCG  
 CCGCTCCCGCCGCCCGAGCCTGGCATCCAGAGTACGGGTGCGAGCCCGGGCCATGGAGCCCCCTGGGAGGGCGG  
 CACCAGGGAGCCTGGGCGCCCGGGGCTCGCGCGGACCCCATCGGGTAGACCCAGAAAGCTTCGGGAGCCCTTCG  
 GCACCTCTGGACCGCCAGGATGCTGTGGCCACCTCCTCCTCCTCCTCTTGGAGGGCGCTCTGGCCCATCCAG  
 ACCGAGATTATTTTCCAAATCATGCTGTGTGAGGACCCCGCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA  
 GGCCCTCGGTGGGACAGCGCACCTCCCTGGCCAACTGCACCTGGCTCATCTCGGCAGCAGGAAGACAGACATG  
 TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAAACCTACGCTCCCTCTCCAGCCAC  
 TGATCTCCCTGTGTAGGACACCTCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTACCATCATCTTACAGCTATG  
 CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCTACAGCCAAAGATTGGCTGATGTGCGCTGCAGGAAG  
 AGTTTCAGTGCTGAACCAACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT  
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCCTGACCCAGACCGCTCCCTCCCTGGCTTGAATG  
 TCACCTTGGAGGACTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCGAGT  
 CCTGCCATGGCTGTGGACCCCATGATGGCGGGCGGCTGGCGCTTACAGCCCTGGACTTGGGCTTTG  
 GAGATGCAGTGATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCTAGTCTCACCCACTTCA  
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTGTCTTACCACACAGTGTCTTGGAGCA  
 ATGGTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCCCTGTGGCTTAGGCT  
 CTGGCCCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGCTACAGTGAGGACACAGCGCTGTGACGGCTCATGGGACT  
 GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTCTGGGGCTGCTGGCACCT  
 CTGGTGCCACAGCCTGCTACTCTGCTGTGACCGCTGCAACTACAGACTTCTGTGCTGATGGAGCAGATGAGA  
 GACGCTGTGCGCATTTGCCAGCTTGGCAATTTCCGATGCCGGGACGAGAGTGCGTGTATGAGACGTGGGTGTGG  
 ATGGGCGAGCCAGACTGTGGGAGCGAGCTGATGAGTGGGACTGCTCTATGTTGTGCCCGGCAAGGTCAATACAG  
 CTGCGACTTATGGCAGCTAGTGTGCGGCTGCTCCTGTGTCATCGCCCTGGGCTGCACCTCAAGCTCATTGCCA  
 TTGCGACCCAGGACTACAGACTTTTGGCCCTCTCCCGGATGGAGGCTGAGATGTGCGAGCAGCAGGACCCCC  
 TCTTCTCAGGGCAGCTCATTGCCCGAGGGTCCATCCACCTGTAGAAGACTTTCTCCAGGATATGACTCCAGGAGTGGCCCGAGGT  
 ACTCATGCTGGGGCAACTCTGCTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGTGGCCCGAGGT  
 CCGCGCGTGTGACGGGGCGGCTTGTATGCGCAGCTGGTGTACCGCGCTCCGCGCTGGGGCTTGTCCCTCGAA  
 CCNACCCCGGCTCGGGCTCTGAGGCCAGATCCAGGCTCAACCTCTCTGCTGCTCCCTTGGAGCCCTAGATG  
 GTGGCACAGGCTCAGCCCGTGGAGGGCGGGCAGTGGTGGGCAAGATGGGGAGCAGGACCCCCCATGCCCCATCA  
 AGGCTCCCTCCCATCTGTAGCACTCTCAGCCCCCACTACTGCTCCCTGAAGCCCCAGGGGCCACTGCCCTCAC  
 TGGCCCTAGAGCCATCATATTGTCTGGAGTGGTGCAGGGCCCTGCGAGGCGCGCTGTGTGCCAGCTCCCTACAGGGCCCT  
 CAGGACCAACCCGAGAGCCCTCGAGCCCAACAGCAGTCTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
 TGCACCTGGCTGAGCCGGGGTGTGGGTAGCTGAGGCGAGGGATGAGCCACTGCTTACCTGAAGGGGACCTGGGG  
 CTCTACTGAGGCTCTCCCTGGGGGCTCTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCTCC  
 ACCATTCTTCTTCTCTGGATTTCAGGGACTTGGTGGGCTCCCGTGAACCTATGTAGCTGCTATAAAGT  
 TAAAGTGCCTTCAGGCGAGGAGGGCTCAGAGAGTCTCCTCTGACGTGGCCATGGCCAGACACCCAGTCCCT  
 TCAACACCACTGCTCCCGACGCCACCACTTTGGGTGGCTGTTTAAAAAGATAAAGTCTTAGAGGATCATTA  
 GGTCTGGACACTCCATCTTGGCCAACTCTACCCAAAGTGGCTTAAAGCACCGGAATGCCAATTAACATAGAGA  
 CCTCTGAGCCCAAGGGGAGGATTTGGGAGAACTGAGGTTTGGCCATCCACCAATCCCTCTACAGGGGCTGG  
 CTCACAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGGCATGTCTCAGTAAGTTGAGGTCAAAAATAA  
 GGAATCATACATCTC

0997555.101601

## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPQLPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MQQGFLLSYSQDWLMCLQEETFQCLNHRCSVSAVQRCGDGVDCDGDGSEAGCSSDPFPGTLTRP  
VPSLPCNVLTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSDWCADGTDDEDCPGCPPGHFP CGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPD CADGSD EWDCS  
YVLPKRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQAPP SY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPT TVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGP PGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVVVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

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## FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAA

09978585.101501

## FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMSTFFIIAQAPEPYIVITGFVETVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

#### **Potential type II transmembrane domain:**

amino acids 26-42

#### **Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

#### **Leucine zipper pattern**

amino acids 78-99 and 85-106

#### **N-myristoylation site.**

amino acids 110-115

#### **Ribonucleotide reductase large subunit protein**

amino acids 116-127

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## **FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGNTTGCCGAC

09973585 101604



## FIGURE 72

CAGCCCCGCGCGCCGCGCCGAGTCTGCTGAGCCGCGGCTGCCGGAACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCCGCTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCGCGCCCTTCAAGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCCACCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCGGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCTACATAGACAGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCAGCTGCTGCGCCTGCCCCAGAAGGTGTTTGTATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGTGGACGAATTGCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCTTCCGTATCACAATCCTGCCTCAGCTTTACATTGAGC  
CCATGATGGGGGCCCGCTGAATTATGAATGTTACCGATTGCGCATTTCCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGTGGGCTTCGACAGCGAGCCCCGTGTCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGAATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCTGCTGCTGCTGCCGTTCGGGTGTGAGCGTCGCCCCCGTGACCCCTGAGGTGCTCA  
ATGATGAGTCTCTCTGGTCTGAGCATGCTGGAAATGAATAGCCAGGCCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCTGCTCCAGATGCTTCTAGATTACAC  
TGTCTTTTGATTCTTGATTTCAGGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTA  
AAAAAACTTCATTCTAA

10978585-101301

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493  
><subunit 1 of 1, 518 aa, 1 stop  
><MW: 56180, pI: 5.08, NX(S/T): 2  
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLR  
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYLRDENSRSRFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCGAILLV LIVLLLLPFRC  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

## FIGURE 74

CGCCTCCGCCTTCGGAGGCTGAOCGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCGCCGTCGCGCGGCATGGGAACCTGCGGGGCCGACGGCCGTGG  
TCAGGGCGCCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCCTGAAGGCATGTGCCCTTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCACTGTGCGGGACGCTTGACTTCAAACGCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGGCCCGGAGCTCGCCAACAGCAGCTTGAGGCCACTGGCGTCACTGCTATGCAGCCACC  
CAGGGCCTGTGAACCTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGAAG  
AGGTGCCTCCAGCTGCCGAGACGACCGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTTGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGAGGACTC  
AGAGGCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTTCATGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACATGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGCTCTCACAGTGAGTAGGAGGAGGCCTG  
GGATCTGAACCCAAGGCTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAA

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## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGTAVVTGANSIGIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRNVNIGPPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTYAAHPGPVNSEFLRHVPGWLRPLLR  
PLAWLVLRAPRGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHRLWEASKRL  
AGLGPGEAEPDEDPOSEDSEAPSSSLTPHPPEPTVTSQPYSPQSSPDLSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

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## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA14104  
<subunit 1 of 1, 985 aa, 1 stop  
<MW: 105336, pI: 6.55, NX(S/T): 7  
MGGMAQDSPPQILVHPQQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAESDEGYTCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPAVWLSWKV  
SGPAAPQASYTALFRTQTAPGGQGAPWAEELLAGWQSABELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLRLPEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRTSBDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARPLDCRRSLLSWDSRSPGVPLLPDTS  
FYGSLIAELPSSSTPARPSPQVPAVRRLPPQLAQLSSPSSSDSLCSRRLSSPRLSLAPAEA  
WKAKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS  
SSNELVTRHLPAPLPHETPPTQSQQTPPPVAPQAPSSILLPAAPIILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLFEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPDPDSQISSQRSQLHCRMPKAGASPVVDS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753



## FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196  
<subunit 1 of 1, 332 aa, 1 stop  
<MW: 36143, pI: 5.89, NX(S/T): 1  
MRLLVLLWGCLLLPGYEALEGPPEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLDQAGEYWCVEKRGPD E SLLISLFV  
FPGFCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG  
TSQYGHERTSQYTGTS PHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
VISMPPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128



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TTTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGAGCTCAGGGGTGCACCTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCAAGGAGGCTGGTGAGCTGCCTGTATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGTCTGCCTTGC  
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCAGATCAACAGCCGAGGTGGTGCAGCAACCTCACCCGAAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAGGAAGACTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGAACTGGGAATGTGTTTGGTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGTTGAACGTGAAA

## FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187  
<subunit 1 of 1, 146 aa, 1 stop  
<MW: 16430, pI: 5.05, NX(S/T): 1  
MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGCDF

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **N-myristoylation site.**

amino acids 67-72

#### **Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

007535.0301

## FIGURE 82

AGCCGCTGCCCGGGCCGGGCGCCCGCGGCGGCACCATGAGTCCCGCTCGTGCCCTGCGTTTC  
GCTGCGCCTCCTCGTCTTCGCGCTTCTCAGCCGCGCGAGCAAAGTGGCTGTACCTGGCCA  
AGCTGTCGTCGCTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGCCCATTTGAGGAGTGCCAGTACCAGTTCCGGAAACCGGCGCTGGAACTGCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGTGGGGAGCT  
GGAGAAGTGCGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAAATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGGCAG  
GAAGGCCATCTGCACACATGCGGGTGAATGCAAGTGCCACGGGGTGTCAAGGCTCCTGTG  
AGGTAAAGACGTGTGCGCAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGCGGCACGAGGGGCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGCGCCGCGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCAGTGTGCTGCTTCGTCAGTGCCGGC  
AGTGCCAGCGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACACCTACCCCAAGA  
GATACTGGTTGTATTTTGTCTGCTGTTGGTTTTTGGGTCCCTCATGTTATTTATTCGCGAA  
ACCAGGCAAGCAACCCCAAGGGCAACCAACAGGGCCTCCCCAAAGCCTGGGCCCTTGTGGCT  
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCATAGGCTACTGACCGTGTGCATCGGGGAAGAGGGGGCCTTATGGCAGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACAGGTCAGGGCACAGGTCATTTACAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTCTCAGGCAAGAAGAGGAGATGAGAGCAAGAGACGACTGAA  
GTCCACCTAGAACCCAGCCTGCCCCAGCCTGCCCTTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACAGGGATCCCGGCTGTGCCTT  
TGCACTCATGCCCAGTCACTTTTACAGCGCTGTTCCTCATGAACTGAAAAACACACAC  
ACACACACACACACACACACACACACACACACAGGACACACACACACCTGCGAGA  
GAGAGGGAGAAAGGGCTGTGCCTTTGCAGTCATGCCGAGTCACCTTTACAGCACTGTTCTCT

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328  
<subunit 1 of 1, 351 aa, 1 stop  
<MW: 39052, pI: 8.97, NX(S/T): 2  
MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILLTHMRVECKCHGVSGSEVKTWCRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCCKFWCCFVKRCQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

0975525-101501

## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGAACACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGGTC  
ACCACAGTCCCTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCTCGAAGCAGACGGCGCGCTGG  
GTGCCCTGAAGGAGGAGGTCGGAGACTGCCACAGCTGCTGCTCGGGACGCGAGCGCAGCTG  
CAGACCACGCGCGCGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGCCGCTGGTTACTGGCTGGGCCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTGAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACAGGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTCATGATGC  
TGCACACGGGGCTGTGGAACGACGACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTCTCT  
CATCCACCGTGTCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCAGTGCC  
TGGGCTCTGGGACCTCCATGCGACCTCATCCTAACTCCACTCAGCAGACCCAACTTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

## FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352  
<subunit 1 of 1, 293 aa, 1 stop  
<MW: 32562, pI: 6.53, NX(S/T): 2  
MDTRYSKWGGSSSEVPGGFPWGRVWHSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLRLTNASKQTAALGALKKEEVGDCHSCCSGTQAQLQTTRAEALGEAQAKLMEQESALR  
ELRERVITQGLAEAGRGREDVRTTELFRALAVRLQNNSCPEPTSWLSFEGSCYFFSVPKTTW  
AAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

097355-10160

## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCCAGTCTTATCTGCCTCTCG  
CTGGAGGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAATAAGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAAACCCAGCCCGCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGCGCCGCGCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTACGGGCAAGTGGAGGCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCGCCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGCGGAGGCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCACGCGCAGGCACTCGTGGTCTCGTTTGTGGTGCATCGTGCC  
CAGCCCCGACTGGTTCTGGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGCGCGG  
AACAGGCGCGCTGGACCTGTACCCCTACGACGCGCGGACGACAGCGGCTTCACTTCTCC  
TCCCCCAACTTCGCCACCATCCCCGAGGACACGGTGACCGAGATAACGTCTCTCTCCAG  
CCACCCGGCCAACCTCTTACTACTACCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGTTGA  
CACTGTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCAGTCTTGCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGTCGTCTCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGTCCAGCCCGCCAAACACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG  
GCTGAGTGCCTCCCTGATAACTGCGCTTAAGACACAGAGCCCCGAGCCCCCTGGGGCCCCCG  
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCGGCGACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCTGCAGGATAAAGTCATCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTGCTCCAGGAGATTGTCTTTCATCG  
TCCAGGGGCTGTGGCTCCACGCTGGTTGCAGATACCTCAGACCTGGTGTCTAGGCTGTGCTG  
AGCCCACTCTCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAA

CGG7657.40300

## FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971  
><subunit 1 of 1, 331 aa, 1 stop  
><MW: 35844, pI: 5.45, NX(S/T): 2  
MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAHSSDYSMRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWVFGVDSLDCGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLRLRQSP  
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA  
NNGSPCPELEEEAECPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

00766610101



## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGC GTGA  
TATTGACAAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGTA CTCTG TAGGCGGA  
CAGCTTTAGTGGCCGGCGCGCGCTCTCATCCCCGTAAGGAGCAGAGTCC TTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCTCCACGAATGGGAAGGTTT TATTGAAACTA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAAC TTTGTTTGGGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTCA TTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTTCCAAGGGAAATTAAAGGCTGAAAAAAGA  
GAAACCAGAGGAGGAAGTAAGAAATTAAGAAACCAGGACACAAAAATTTTAGTTTACTTTT  
CATTGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCAGT  
TG TAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA  
TTAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGAGTGAAAGAGCTCAGAAAAGAAGCAAGCAATTAAACGGGAACCTTAGCAG  
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAGTGAAGAGGAAGAA  
GCCCTCCAGATGGTGCTGTTGCGGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAAC TTTCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAAGGAGGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAAACAGCCATTG  
TTCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTGTG  
AAAAACAATTATCTTGTTTTGCAAATTTGTGAATGATGTAAGCAAAATGCTTTTGTTACTGG  
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCCT  
TCCACAAAAA

## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919  
><subunit 1 of 1, 472 aa, 1 stop  
><MW: 53847, pI: 5.75, NX(S/T): 2  
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPDDIIPREIKRLKKEK  
PEEEVKKLKPKGKTNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKCLKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVA EYRREKQKYBALRK  
QQSKKGTSREDQTLALLNQFSKLTQAIAETPENDIPETEVEDDEGWM SHVLQFEDKSRKVK  
DASMQSDTTFEYDPRNPFVNKRRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

## FIGURE 90

CGCGCCGTTGGGGCTGGAAGTTCGCCAGGTCGTCGCGGCGAGAGAGATGCTGCCCG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGTGTACGCGGCTCG  
AGCCCTGGCCAGACATGTCCTCCACAGGGTTCTCCTTCGGGTCGCGGACTCTGGGCTCCACCACC  
GTGGCCGCGCGCGGACCAGCACAGGCGGCGTTTCTCCTTCGGAACGGGAACGCTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGAAATCTTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGGTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATA CAGGTGCCTTGCACACCAGAGGCTCAAGTGGTCACCAATATGGAAC  
CTTCGAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCTGTCAGGAGTCTCTGGGCGCAGCTGGCCTCG  
ATGTACGTGACGACGCGGGAACGGTACAAGTGGCTGCGCTCTCAGCAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCCGGGATCCGAGTGCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTCACTGTGGGCGCTGCTTCTTCGTACAGGGCTCTGACTTGCGCGCCCGC  
GAGAAAAGTGGTCTGGTGTCTTCGACGACAGGCTCGGCACTCTTCGCTTCTGAGCACGGA  
CGACAGCCACGCGCGGGAACTGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCAGGAAATGTGACCCCTGTTCCGCCAGTCCGCG  
GGGCGCATGAGCATCTCAGGACTGATGATGTCACCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCCAGAGTGGCACCGCTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAACT  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCAGATGACCTTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATACCAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGATGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAGATGCCACTTTCGTGTATGCCCACTGCAGACTGCTCAC  
TACCACCGAGAACCCCAATGATGGGAATCTGCCCTGTGCGCCACGCTCAACAAGGATGAA  
AAGTACCTGCGAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAGAGGGGTTTGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGAAGAAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCACTGCCCTTTCAGCC  
TGACATCCCATGATGCCCTCTACTTCAGTGTGACATCCAGTTAGGCCAGGCGCTGCAAC  
ACCACCTGTGCTCAGCTCTCCAGCCTCAGGACAACTCTTTTTTCCCTTCTTCAAACTCT  
CCACCCCTTCAATGCTCTCTGTGACTCTTCTTATGGGAGGTGACCCAGACTGCCACTGCT  
CCCTGTCACTGCACCCAGCTTGGCAATTACCATCCATCCTGTCAACCTTGTTCCTGTCTGT  
TCACATTGGCCTGGAGGCTTAGGGCAGGTTGTGACATGGAGCAAACTTTGGTAGTTTGGGA  
TCTTCTCTCCACCACTATCTCTCCCCAGGGCCACTCCAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

## FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG  
FGTGLFGSKPATGFTTLGGTNTGALHTKRPQVVTKYGTLLQKQMHVGTKPIQVFLGVPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTFLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFPQRDPEEIIWSMSPVVDGVVIPPDD  
PLVLLTQQKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD  
IVQDATFVYATLQTAHYHRETMMGICPAGHATTRMKSTCSWILPQEWA

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Carboxylesterases type-B serine active site.**

amino acids 312-327

#### **Carboxylesterases type-B signature 2.**

amino acids 218-228

#### **N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

09/555/2016

## FIGURE 92

GAGAACAGGCCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATATGCTACTGCCACTGCT  
 GCTGTCCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGGCAGG  
 AGTCAGTGATGGTGGCGGAGGGCCGTGTCATCTCTGTGCCCTGCTCTTTCTCCCTACCCCGCA  
 CAAGACTGGACAGGGTCTACCCACGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
 CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAATGAGCACC CGGGGCC  
 GATTCCAGTCACTGGGGATCCCGCAAGGGGAAGTGTCTCTGGTGATCAGAGACGCGCAG  
 ATGCAGGATGAGTCACAGTACTTCTTTGCGGTGGAGAGAGGAAGCTATGACATATAAATTT  
 CATGAACGATGGGTCTTTTCTAAAAGTAAACAGTGCTCAGCTTACGCCGACCCAGGACC  
 ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
 GTCGAGTCCGTGTGGCCTATGCCCCACAGAGACTTGTATCAGCATTTACAGTGACAAACAC  
 GCCAGCCCTGGAGCCCCAGCCCCAGGGAATGTCCATACCTGGAAGCCCAAAAGGCCAGT  
 TCCTGCGGCTCCTCTGTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGAC  
 AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
 GGTGAAGGCTGGGGATTACGGGCGCTACACCTGCCGAGCGGAACAGGCTTGGCTCCCGAG  
 AGCGAGCCCTGGACCTCTCTGTGAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
 GCAAAACGACAGCTCTGGAAACCTTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCA  
 AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
 GGGGACAGGTTCTGAGCCCCCTCCAGGCCCTCAGACCCCGGGTCTGGAGCTGCCTCGGGTT  
 CAAGTGGAGCAGGAAGGAGAGTTCACTGCCACGCTCGGCACCCACTGGGCTCCAGACAGT  
 CTCTCTCAGCCTCTCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
 CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTCTCTGCTGGCCTGATCATCATGAAG  
 ATTTCTACCGAAGAGACGGATCCAGACAGAAAACCCGAGGCCAGGTTCTCCCGCACAGCAC  
 GATCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
 AAGCCACACCAACAGTCCCTCGGACCCCTCCTCCACAGGTGCTCCTCTCCAGAAATCAAAG  
 AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC  
 CCCAGAATCCAGGAGAGCCAAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGGCTCA  
 GACCCAGGCTGAGGCCCGGATGCCAAAGGGCACCCAGGCGGATTATCGAGAAGTCAAGTTC  
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
 GTTGAAGATAACAGAGTGCAAAGTTCTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCCTGTAATC  
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGGTTGAGACAGGACCTG  
 GCCAACTTGGTGAAACCCGCTCTCTACTAAAAATACAAAATTAGCTGGGCATGTTGGCAGG  
 CGCCTGTAATCTTACTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
 AGGTTGCAGTGAGCCAAAGTACACCATTTGCACGCCAGGCTGGGCAACAAAGCGAGACTCCA  
 TCTCAAAAAAAAATCCTCCAAATGGGTTGGGTGCTGTGTAATCCAGCACTTTGGGAGGCTA  
 AGGTGGGTGGATTGCTTGAGCCAGGAGTTCGAGACAGGCTGGGCAACATGGTGAACCC  
 ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGCTGGCTGTAGTCCAGCTGT  
 CAGACATTTAAACACAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
 TACTGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
 TACAAGATACAGGTCAATAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAACCCAAAG  
 ATCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGTGCTCTCACTGCTACACTCCT  
 GACAGCCCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
 AAAGGGGAGGAATGAATAATCCACCCCTTGTGTTAGCAATAAAGCAAGAAATACCATAAAA  
 GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTGTCTCTT  
 TACTTTCTTAATAAATCTGCTTTACCTTAAAAAAA

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 60268, pI: 9.53, NX(S/T): 3  
MLLPLLLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSTPRPQDHNTDLTCHVDFSRKGVSQARTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 399-418

#### **N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

### **Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

# FIGURE 94

TGAAGAGTAAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT  
 TATGTTGGGAATTCCTCTCCTATGGCCTTGCTTGGAGCAACAGAAAACCTCTCAACCAAGA  
 AAGTCAAGCAGCCAGTGGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGGGAACCAATTT  
 TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
 CAATGGAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGCATCCCTC  
 TACATCTTAAAGAGCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAAACCTGAGTCTGA  
 GTTTGTCTCAAAAGTTTCGGATATCAATGACAAATGAACCAAAATTCCTAGATGACACCTTATG  
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
 ATATTTTTCTGTTGAACCAACACAGGAGTCATAAGAATATCTTCTAAATGGATAGAGAAC  
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
 TCTGGAACAACAAGTGTTAATTAATACTTTCAGATGTTAATGACAATAAGCCTATATTTAA  
 AGAAAGTTTATACCGCTTGACTGTCTCGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
 TCATGGCATATGATAATGACATAGGAGAGAAATGCAGAAATGGATTACAGCATTTGAAGAGGAT  
 GATTGCGAAACATTTGACATTATTAATACTAATCATGAAACTCAAGAAGGAATAGTTATATTA  
 AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
 ATGTTCCGTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCATTTCTTAAATAGATCCAG  
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTCATATTATGATTATTGAAGTTTTTGA  
 AGAAACCCACAGGGATCATTGTTAGGCGTGGTGTCTGCCACAGACCAGACAATAGGAAAT  
 CTCTCATCAGGTATTCTATTACTAGGAGCAAAAGTGTTCATATCAATGATTGGTACAATC  
 ACTCAAGTAACCTCACTGGATCGTGAATCAGTGCCTGGTACAACCTAAGTATTCAGGCCAC  
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCATGTATGTGCAAGTTCTTAAACATCA  
 ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGACGGCTCT  
 GGTGAGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
 TTACTTTAATCTATCTGTAGAAGACATAACAATTCAGGTTTACAAATCATAGATAATCAAG  
 ATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
 TACATCTCCATCTTAATTTGCCGACAATGGAATCCCGTCACTTCAAGTACAACACCCCTTAC  
 CATCCATGCTCTGTGACTGTGGTGACAGTGGGAGCACACAGACTGCCAGTACCAGGAGCTTG  
 TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA  
 TTTGGGTTTATTTTTTGACTTTGGGTTTAAACACACGGAGAAAACAGATTCTATTCTCTGA  
 GAAAAGTGAAGATTTTCAAGAGAAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
 ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATCGGGGAACGCAAGACT  
 CGGAAAACCAACAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
 CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATCTGATCCGTGTG  
 CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGGGGAACAGGGTCATTAGCTGGATCC  
 CTGAGTCTCTTGAATCAGAGCTCTGATCAGGATGAAAGCTATGATTCTAATGAGTT  
 GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
 GCTTTTACCATCAAATTTTTTAAAGTGCTAATGTGTTATCGAACCAATGGTGTGCTTAA  
 AGAGTTTTGTGCCCTGGCTCATTTGCGGGGAAGCCCTAGTCTATGGAGTTTCTGATTTC  
 CTGGAGTAAATACTCCATGGTTATTTTAAAGTACCTCATGCTGTGATTGAACAGAGATGTG  
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACAGGATTTGAAGTAAATAATG  
 TAGGAAGATATTAAGATGATGAGAGGACCAAGATGTAGTCGATCCTTATGCGATTATAT  
 CATTATTACTTTAGGAAAGAGTAAAAATACCAACGAGAAAAATTTAAAGGAGCAAAATTTG  
 CAAGTCAATAGAAATGTCAAAATCGAGATGACATTTTACATTCTCATATGATGACATGAA  
 ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT  
 TTAATA

09976535-101601

## **FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSRLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLNNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAVIDIAT  
GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD  
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIIEQISSIPLYVQVLNINDHAFEPFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVDCDGSSTQTCTCYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSGLAGSLSSLESASVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254



## **FIGURE 96**

ATTTC AAGCC AGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTCGCAAAACATTGACATTATT

09070805 101001

# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGGCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGCGCGCAGCGAGCAGGGCTCCCGCCCTTAACCTTCTCCGCGGGG  
CCAGCCACCTTCCGGGAGTCCGGGTTGCCACCTGCAAACTCTCCGCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCATGGCCAAACGCGGGGTGCAGCTGTTGGGC  
TTCATTCTCGCTTCTCTGGATGGATCGCGCCATCGTCAGCACTGCCTGCCCGAGTGGAG  
GATTTACTCCTATGCGCGGCACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCTGCGCTGTGCGACAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCAATTGCAAGCAACCGTGCTTGTATGGTGGTGGCATCTCTCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCTATTGGGGGTGCGATATTTCTTCTTGCGAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAAATCGTTCAAGAATTCTATGACCCCTATGACCCGAT  
CAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCT  
TCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCTCCCGAAAAACAACCTCTTACCCAAACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGCACACAGAGGCAAAAG  
GAGAAAAATCATGTTGAAACAAACCGAAAAATGGACATTGAGATACTATCATTAACTATGAGC  
CTTAGAATTTGGGTATTGTTAATCTGAAGTATGGTATTACAAAAACAACAAACAAAA  
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA  
ATATAGGAGGGGAAGATTTTCCATTGTTATTACTGCTTCCCATTTGAGTAATCATACTCAAA  
GGGGGAAGGGGTGCTCCTTAAATATATAGATATGATATATACATGTTTCTTATTA  
ATAGACAGTAAATACTATTCTCATTATGTTGATACCTAGCATACTTAAATATCTCTAAAT  
AGGTAATGTATTTAATCCATATTTGATGAAGATGTTTATTTGGTATATTTCTTTTCTGTC  
TTATATACATATGAACAGTCAAATATCATTACTCTTCTTATTAGCTTTGGGTGCTTTG  
CCACAAGACCTAGCCTAATTACCAAGGATGAATTTCTTCAATCTTTCATGCGTGGCCTTT  
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCACTGTTTATTAAGCCCTTAT  
TTGTTTGTGTTTCATTGGTCTCTATCTCTGAACTAACAATTTATAGCTTACATTTTA  
GTTTCTAAGCCAAGAAGATTTTATCAAAATCAGAACTTTGGAGGCAAACTCTTCTGCATG  
ACCAAGTGATAAAATTCCTGTGACCTTCCCAACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCGAATGAGTAGCTGCATGCTGTTCCCGAGGTGTGTT  
AACACAACCTTATTTGATTGAATTTTAAAGCTACTTATTCATGTTTATATCCCTTAACT  
ACCTTTTTGTTCCTTCTTAAATTTGTTTCTTCCCAAGTGAATTTATCATGCGTTTTTA  
TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTACCTCTTT  
TTCTATCTGCCAAATTGAGATAATGATACCTTAACAGTTAGAAGAGGTAGTGTGAATATTA  
TAGTTTTATATTACTCTTATCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT  
CTAGCTGGCTGAGACATGAAGAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATT  
CACTGCCCTCTCTCTACCACTGCTATTTCCACTGAACAAACCTACACACATCTTCTAT  
GTGGTTGAGTGCCTTCTCTCTCTACCACTTATTTCCACTGATCTGCTGCTGACGACATAC  
CTTCATGCGCTCAGTGCCCTTCTCTCTCTACCACTTATTTCCATTCTTTCAGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAAACAAGTCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCTTGAGCAAGATGATGTAATGGAAGGCTGTTGGCTGCTGCTGGAGCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTGAGCAAGGCATTTGGCTGCTGTA  
GCTTATTGCTTCATCTGAAGCGGTGGTTTGTAAATCCTGATCTTCCACCTCACAGTGATG  
TTGTGGGGTCCAGTGAGATAGAATACATGTAAGTGTTGTTTGAATTTAAAGTGCTAT  
ACTAAGGGAAAGAAATGAGGAATTAACGTCATACGTTTTGGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

00976565.101601

## **FIGURE 98**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 22744, pI: 8.51, NX(S/T): 1  
MANAGLQLLGFI~~L~~AF~~L~~GWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCV~~S~~QSTGQI  
QCKVFD~~S~~LLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMPVPVNARYEFGQALFTGWAASLCLLGGALLCCSC  
PRKTTSYPTPRPYPKAPSSGKD~~Y~~V

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

007055-101601

100%  
 90%  
 80%  
 70%  
 60%  
 50%  
 40%  
 30%  
 20%  
 10%  
 0%

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCTCTGGGATGGATCGGC  
GCCATCNTCACTGCCCCTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCAGCCCATGTACGAGGGGCTGTGGATGTCNCNGCTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCA TTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAA  
NNTTCAACANTTCTATGACCCATGACCCAGTCAATGCCAGGTACGAAATTTGGTCA  
GGCTCTCTTCTACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCTGTGCC

## **FIGURE 100**

ACCCTTGACCCAAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGAAGACGATGA  
GGTGCGAAGATGAGGATGGCTGTCAATTGGGGCGCGATATTTCTTCTTGCGAGGTCTGGCTA  
TTTtagTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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## **FIGURE 101**

GGGCCCACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCAGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCTT  
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCCTGCGA

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09970535-101604

ATTCTCCCTCCTGGATGGATCGCNCACCGTCACATTGCCCTCCCCCANTGGAGGATTNAC  
TCCATATGCTGGCGACAACATCGTAGCCCCCAGGCCATTACCGAGGGGGCTTTGGATGTGNT  
GCNTGTGCGAGAGCACCGGGGAGATCCCAGTGCAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCGCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTGTTGCAGGCTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGACTNNNTCANNNNNTCTATGACCCCTATGACCCCGAGTCAATG  
CCAGGTACGAATTCTTGTCAGACTCTCTTCCAGCTGGCTGGGCTGCTGCTTCTCTCTGCCCTCTG  
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

## **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTG CAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTCTGTCCCGAA

007655-10360



## **FIGURE 104**

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCTATGNTGGGACAAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAGA  
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTCTGCGAACC

007055110101

## FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGINTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTGCTGTTCCTG

0978585.101001

## **FIGURE 106**

TTCTCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCN TGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGGAAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCGAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGTCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

00070505.101601

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCTCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCATGGAGGATTACTCNTATGCTGGCGCAACACATCGTGACCNCCCAGGCCA  
TGTAACAGGGGGCTGTGGATGTCNCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNATGCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTTGCGAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTTCTTCTG  
AGGCTTGCTGCTATTTNAGTTGCCACGATGGTATGGCAATGAAGTCGTTCAAGAATTCTAT  
GACCCATGAGACCCAGTCAATGCGAGGATCGAATTTGGTCAGGCTCTCTTCACTGGCTGGC  
TGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGAA

## FIGURE 108

GC GTGCCGT CAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCAC  
CGCGTAGACGACCCCCCCTCCAGCGCGCCCCACCGGTAGAGGACCCCGGCCGTGCCCGG  
ACCGGTCCCCGCTTTTGTGTA AAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCGGT  
GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCCGCTAAGGAACTGGCGAAGGTGGAG  
CAGGTCTTGAGCCTCGAGCCG CAGCAGAGCTCAAATTCGAGGTCCCTTACCAGTGTGTG  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATCAGGGGCCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAGTAAACA CAAGTT  
TATGTTTCAGTCTATGTTTGTCTCCA CTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAAATGCCAGCAGAGAAT  
GATAAACCATGATGTAGAAATAAATAAAATATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTCTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTT CAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTT CAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTGTCTTTA  
TCGTTGGTGTAATTATTTGGGAAGATTGCCTTTGAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTA AAAAGAAAT  
AATGTATGATGACATCTCACAGGTCTTGCCCTTAAATTAACCCCTCCCTGCACACACATACAC  
AGATACACACACAAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAAGATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAATGTCA TTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCTTCTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT  
GCTGGGGAGTGCGGT CAGCTCCACACAGTAGTCCCAACGTGGGCCACTCCCGGCCCAGGCTG  
CTTTCGGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTCTCACTTAAAGGGACCAA  
GCTAAATTGTATTTGTTTCATGTAGTGAAAGTCAAACCTGTTATT CAGAGATGTTTAAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCA GTTTTTCTTATTGT CACAAGAGTACAGTTAATGC  
TGCTGTCTGCTGAACTCTGTTGGGTGAAC TGTGATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGTTGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTCTGGGT CAGTAAATAACAACCTGT CATAGGGAGGGGAAATCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTA CTCACTTCCAGCGCC CAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTT CAGCGAATCTTCTAGTAC  
TAGTTGAGAGTTTGACGTGTGAATTAATTTATGCCATAAAGACCAACCCAGTCTGTTTGA  
CTATGTAGCATCTTGA AAAAGAAAATTTATAATAAAGCCCCAAAATTAAGAAA

00756610601

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHLEKFRGPFTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSDEAVWKEAKPEDLMDSKLRVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

**Important features:**

**Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

007266102614

## **FIGURE 110**

GTCACTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTGTGCATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

09976585.101604

## FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

0978665.104604



## **FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

09/05/2014 10:10:59

# FIGURE 113

GGTGGCCCATTCOCGGCCAGGCTGCTTTCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAAGTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCCTTGGAGAGTCTGGTCATGTGGAGGTGGG

109101.58582660

## FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGCAAGAGTACAGTTAA  
TGCTGCGTGC

09978585.104501

## FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANCTCC  
GGCCCAGGCTGCTTTCGGTGTCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTCAINTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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## **FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

0973585.103604

# FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA  
 GGCTCCAGCTGCAGCGTCCCCGCCCGCCTCTCCGGGAGCTCTGATCTCAGCTGACAGTGCC  
 CTCGGGGACCAACCAAGCCTGGCAGGGTCTCATTCTTGTGGCCAGGCTGGAGTTCACTGCCA  
 TGATCATGGTTTACTGCAGCCTTGACCTCTCGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
 CTACAGGACAAAATTAGAAGATCAAAATGGGAAAATATGCTGCTTTGGTTGATATTTTTCAAC  
 CCTGGGTGGACCTTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
 GGTACCCCGGATTGTCACTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
 CTTTCTGAAATGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGGAACCTT  
 AACAGGGGTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCAGAAAGGGAG  
 TATCTGTGTAGGAGAAAGAGACAGGTGTATGGCACCCGACAGCAGGTTGAGCATCTTGGACAAA  
 AGGTTCTTAACCAATTTCCCTTTTACGACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
 TCTCAATTTCCCTCAGCATGTTCTAAGTGTGCTCCACTGTGTTTATGATGGAAAGGACTATG  
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
 AAACGTGCGAGTTCTAAGAGGAGCAGGAGGAAGCTAGTGGTGGTGACCAAAGAGAGGGGTAC  
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAAAAATCTGGCCGGGGTTC  
 AGAGGATTGCCGAAGGGAGGCCCTTCTTTTCACTGGACCCGGGTCAAGAATACCCACATTCCG  
 AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
 GCTGAAGCGTGTCTCAAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
 TGCCCTGGTGAATGATCCACTTCTCAGGATTGTGATAACGATAGGGCTGATCAGTTGGTCTAT  
 CGGTTTTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACGCGATGCTGAGTC  
 GGGCTCCACCGGTTTCGGGGGTCTATCTGCGTCTGAAGATCCAGACAAAAAGAATTGGAAGC  
 GCAAAATCATTTGCGGTCTACTCAGGGCACCACTGGGTGGATGTCCACGGGGTTTCAAGAGGAC  
 TACAACGTTGCTGTTCGCATCACTCCCCTAAAAATACGCCAGATTTCCTCTGGAATTCACGG  
 GAACGATGCCAATTTGTGCTTACGGCTTAAACAGAGACCTGAACAGGGCGGTGATCATCTAAA  
 TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCGGACTT  
 GAACCTCTGCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCATTTAAAAAA  
 TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTCAATGCCAAGTATATACTCTTCTTTA  
 CATGGTGTAGGTTTCAATTTGTAGAAAAATTTTGTGTCCTTCTAAAAAATTAGACACACTTT  
 AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
 TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
 GGTAGATGGTAAAGCAATTAGTATCAGAAATAGACAGAAAGTTTCAACACAGTTTGTACTA  
 CTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGCT  
 GGGACATTTAGTTTAGTTTTTTTGAAGAAATTCAAATCAGAAAGAAAGCAAGCATTATATAA  
 CAAAATAAATCTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTAAAAA  
 TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAATAAGGGAAGCTGAGACATTT  
 TAAGATCTCAAGTTTTTATTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
 AAGACACTTCACAAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTATGCTATACAT  
 TCTATGTATGAGGTGCTACATTTTAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT  
 CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGCTGAATTTCTCTGATTAG  
 TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

10973565-10973566

## FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253  
<subunit 1 of 1, 413 aa, 1 stop  
<MW: 47070, pI: 9.92, NX(S/T): 3  
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSIILDKRFLTNFPFSTAVKLSTGCSGILIS PQHVLTAACHCVHDGKDYVKGSKKLRV  
GLLMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGORIAEGRPS  
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKMPGGMIHFS  
GFDNDRADQLVYRFCVSVDESNDLLYQYCDASGSGTSGGVYLRLLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGAATGTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGAGCGCCTATGGGATGCGTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCCTCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACACCCATGTTCACTCA  
AGTGCCAAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTAGC  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCCGTCAAGGAAGATAACTGTGGGGCTGCAACCGGAGATGGGTCCA  
CCTGCGCGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTCTGATCACTT  
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTTCGTAACTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTCTTTTC  
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCTTCCCTCGGTGGGAGGCCACCCCATGGACCGCTGCTCCTCC  
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGACATCCAGGGGCA  
TGTCACTTTCAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGTCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCAAAAAACAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGTCTATA  
AACCACAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTTAAGTTGTAAGGACACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGA  
ACTAAGTGTAAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAA

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## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAGPWSECSRTC GGGASYS LRRLCS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDN PCSLKQCQ  
AKGTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGP D HLYLETKTLQGTKGENSL SSGTFTL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPI IHRWRETDFFPCS  
ATCGGGYQLTSABECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVT CGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKLPVEAKLPWFKQAQELEEAAVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGTTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCGCGGTTCTGTGGGCCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGTGATCACCGGGGCGAACAGCGGCTTGGGCCGCGCCACGGCCGCGG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTGTATTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAGTACGCCCGCCTTAGAAGGCACAAATGTACCGTCAATGTGTGATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCAGACTTCCATTTATTT  
GGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGTACTTTGGGGATTGTAAGAGGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTGTACTTGAAGAAAAAGATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTTAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATA  
GTACAATGAAAAATACAAATTATTTGTAATAATATACTGGGCAAGCATGGATGACATATTA  
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELQRQAACGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHIGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGNTVTVNVLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

## FIGURE 123

GGGGATTGTAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

0997885.10151

## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCCAGCC  
CTTTCCTAACCCCAACCCAACTAGCCAGTCCCAGCCGCGCAGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCAATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCTGGTAACTTGGGTTTTTACTCTGTAACTGAAATAACAAGTCTGTCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAATGAAATCAAGTAGTGTGTCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACCTCTTGATCGCAGCAAAAGAA  
ATATCATTTGATATTTTGGAGCAAAAGGACTCGGACAATATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTCTGCATTTGGGGATGTTTCAAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACGAGGCTTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTT  
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC  
AATTAATAAGTAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTG  
TATTTGACTTACATTTCTGAAAACTGCACAGAGAATTCATCATGGACCTGACCCAACCTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAATTG  
AAAAACAGTTTGTAAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTTCTATGTGTATTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

109101-109101

## **FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVTFPVTTETITSLATENIDEILNADVALVNFYADWCRFSQ  
MLHPIFEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMCREYR  
GQRSVKALADYIRQQKSDPIQEBIRDLAETITLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI  
TFENGEEELTEEGLPFLILFHKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFHRMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

0097585-10601

## FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCCAACCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

05978585.101601

## **FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCCGCCGCGAGCCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCTTAACCC  
AACCCAAACCTAGCCCNCTCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

09978585.101604



## FIGURE 128

GCCCCACGCGTCCGATGGCGTTTCACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTGGCACATTATAGCATTGTATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCTGTTTCTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA  
CTCTATGACCCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAAATTTGCAGG  
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

097855.10601

## FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAEWLTLGLNMPLLAYHIWRYMSRPVMSGFGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFFYLYGMIYVLVSS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Type II transmembrane domain:**

amino acids 11-31

#### **Other transmembrane domain:**

amino acids 57-77 and 123-143

00978555-101601  
109101-2358660

## FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCCTTGTA TACTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

00070505-101601

## FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATTGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTGTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTGCAAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGAATGTGAATCTGCATGTACA  
GAAGCATATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGTTGCCAGAATCAGCTGCC  
ATTTCGCTGAAGTGAACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTTTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATCCACTCCTCATAGAGCTTTTAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

09/25/85 10:16:01

## FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP  
KEEELYACQRG CRLFSICQFVDDGIDLNR TKLECSACTEAYSQSD EQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQS FITSSWTFY LQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

09378586.103601

### FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG  
TGAAGTGAACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

10978535-101604

## FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCGGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTGAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTGAGAGAGTTG  
CAGGCTGTTTTCAATTTGTGAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTCGAGAAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCAATCTGGAGTGACATGATGGACT  
CCGC

099101.58587460

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCCTGGGAGGCGGCCCGGAGGT  
GGGGCGCCGCTGGGGCCGCGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTTGATAGATTTAATACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTGATGGAATTAATCTGCGAGCTACAAGTATTTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTGAGTCCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCATGCTTGGAAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC  
AGACAATTAAGAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAATGTGCATTGAGTGAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTGTGATGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAAACAAATGTTACTTCTGGAATACTTCATGAATCAAGTCATTTCCTTTG  
CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGACACAAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA  
AATAGTATCATTATTTCAAGCATTTTGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT  
TCAGGAACCTTGTACAGAATATTCATTTAAGAAAAACAAGCTGATATGTGCTGTCTTCTGGAC  
AATGAGGCGAAAGAGTGGAAATTTCAATCAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

0375581.10561



## FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARQCFCQVSGYLDCTCDVETIDRFNNYRLF  
PRLQKLLESDFRYYKVNLRPCPFWNDISQCGRDCAVKPCQSDVDPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCREADDIQSPEAEYVDLLNPE  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRLKNLYFLYLI  
ELRALSQVLPPFERPDFQLFTGNKIQDEENKMLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

007055 5852550

## FIGURE 137

GCTGGAAATATGGATGTCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTGAGTGCAAGATATCTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTACCATT  
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTTCCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

09975585.101601

## FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAAACAGAAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCCTTCGTCACTCACCTGTTCTTGCCCTGGTGTTCTTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCAGGGCCACCAGAAG  
CTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCCTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCCTCCCAAGCCTGGGAGTAACATATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCTCATTTGCTACCTAATGTGCTTGC AAAAGCTCCATGTTTCTTAACAGA  
TTCAGACTCCTGGCCAGGTGGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCCTCTGCACCTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA  
AATAATAATAATAATAATTAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCAGAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

007055-1050

## **FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039  
><subunit 1 of 1, 124 aa, 1 stop  
><MW: 13352, pI: 5.99, NX(S/T): 1  
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMVS

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Cell attachment sequence.**

amino acids 70-73

#### **N-glycosylation site.**

amino acids 98-101

#### **Integrins alpha chain proteins**

amino acids 67-81

## FIGURE 140

CACAGTTCCTCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTGTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

0070007.2016001

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAAGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTCACAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGTCTCAGATGAAGTGGCCATTTCGCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGTCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCAGACCTCAGCCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTCGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACTTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT  
GGTCTGTGCCACTGTTCTGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCTGG  
TGGTCTCCAGACACCTTGAAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCTGGAT  
CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACTCTGGTCTGCATGACATGGAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAAAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAGTGACTTCACTCCCTTCGGTCTAAGTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCAAGCCCACTGAAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAA

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033  
<subunit 1 of 1, 311 aa, 1 stop  
<MW: 35076, pI: 5.04, NX(S/T): 2  
MQTFMTVLEEIIWTSLFMFFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSL TEGPECDVTDITATVPYNLRVRATLGSQTS AW  
SILKHPFN RNSTILTRPGMEITK DGFHLVIELEDLGPQFEFLVAYWRR EPGAEEHV KMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIP LVLALFAFVGFM LILV  
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

09978535-101607

## FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATT CAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTCGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

0990585.101601



## FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCCT  
GGAGGGACAGGGTCCAGAAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCGAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACCTCGTGCCAGGGCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGAAGCGGCAGAGCCCGTGGATGTGGA  
GCTGAAGAGGGTTCCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACCTACGGGAATTTAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTCT  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGACCCCGCCCTGCTCCGAGACTGTCACTTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCATCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTGCCTGAGACTCCCTTCGAGGATTGCAACCCGCCCTCCTAAGCCTC  
CCCACAAGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGACAGAACTCTTA

09975555-10000

## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDFPLPPLRLSTGGKLRGTLTYNTGRHVSLPAPRFVNVVSGGPL  
LYSHRLSELRLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNRTITRISYKNDAYFLQDLSLELLFPESFGFITTYQGSLSSTPPCSE  
TVTWTILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 177-199

**N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

007553 10507  
10001.5858/60

# FIGURE 146

GGCGCTGGTTCTGCGGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCAGCCTCCGCCGCCGAGCCTC  
 GTTCGTGTCCCGCCCTCGCTCTCTGACGTACTGCTCAGAAACGCTGGGCGCCACCTCTGGCAGACTTAACGAA  
 GCACTCTCCCTCCACCCCAATGTCAGGTCTAATTTTGGACGCTTTGCTCCGCTATTCTTCAGGTTGAGGAGC  
 CGCAGAGGCGGAGCTCGCTATTCTGTCAGTCAGCACCACGTCGCCGCCGAGCAGCTCGGTGTCAGGCCCTTC  
 GCGAGCGGGCTCTCCGCTCTGCGGTCTCTGTGAAGGCTCTGGGCGGCTGCAAGGCGGCCGCTCGGTTTGGCT  
 CACCTCTCCAGGAACTTCAACATGGAGAGCCAAAGAGGTGGAAGAGCCTGTCTTGGAGATTCTCTGGGGA  
 ATCTCAGGTCATTCAATATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACCAAGTGTCTTTCATGGCTAGA  
 GCAATCTCAGCCATGGTGGTCCCAATGCCACTTTATTTGGAGAACTTTGGAATAATACATGGATGGAGTGTG  
 GAGTGGTGGATAGCCAAACAGAGGGAAGAGGCCATCACAGACAATGACATGCAAGTATTTTGGACCTTCAT  
 AATAAATACGAAGTCAGGTGTATCCACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAGA  
 TCTCAGAACTCTGGGCTGAAGTTGCTTTGGGAACATGGACCTGCAAGCTGTCTTCCATCAATTGGAAGA  
 TTGGGAGCACATGGGGAAGATATAGGCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT  
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTGAGGTGTTCTGGCCCTGTATGTACACATTATACA  
 CAGGTCGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAAATTTGTGTCAATACTGAACATCTGGGGGCGAG  
 ATATGGCCCAAGCTGTCTACCTGGTGTGCAATTTACCCCAAGGGAACCTGGTGGGCCATGCCCTTACAAA  
 CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTGGAGGGGGCTGTAGAGAAATCTGTGTACAAAGAGGG  
 TCAGACAGGTATTTATCCCCCTCGAAGAGGGAACAAATGAAATAGAACGACAGCAAGTCAAGTCCATGACACC  
 CATGTCGGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCAATAGCGCACAGCAAGTGTCCCAATTTGTTCT  
 TGTGAAGTAAAGATTAAGAGATCAGTGCAAGGAAACAACTGCAATAGGTACAGATGTCTGCTGGCTTTTGGAT  
 AGTAAAGCTAAAGTATTGGCAGTGTACATTATGAAATGCAATTCAGCAGCTGTAGAGCTGCAATTCATTATGT  
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAGCATTATTTCACTCAAGTCCATAGA  
 AATGGTATTCAACAAATTTGGCAAAATTCAGTCTGCTAATTCCTTCAAGCTCTAAAGTAAACAGTTCAGGCTGC  
 ACTTGTGAACAACTGTGGAACAGCTCTGTCCATTTCAATAGCGCTGTCACTGCGCCCAAGGATCTGCTCT  
 CGTAAGCTGTATGCAAGCAAACTGCACATATGCTCTGTGTAATGGAACTCGAGTGTATCTGATCTGTCCAGTATC  
 TGTGAAGCGCAGTACATCTGGCTGGTGTGAAATCAGCGTGGTTATGTGTATGTATATGCTGTGGACAAAGA  
 AAGACCTACATTGCTCTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAACTCTCAGGAGGAAAGGCACTT  
 AGAGTGTGTTGCTGTGTTGTGAACTGAAATACCTTGGAGAGGACCATAAGACTATTTCCAAAATGCAATTTCTGA  
 ATTTTGTATAAACTGTAACTATTCTGTACAGAGTACATCAACTATTTTCAGCCCAAAAGAGTGGCAAAATGCATA  
 TAACTCTGATAAACAAAGTCTATAAAATAAACATGGGACATTAGCTTTGGGAAAAGTAAATGAAAATATATAGG  
 TTTTGAAGATCTCTGTGTTAAATATTGCTATATTTCTTAGCAGTTATTTCTACAGTTAAATACATAGTCATGATT  
 GTTCTACGTTTCAATATATATATGCTGCTTTGATATGCGCACTAATAAAATGAATCTAACAATTTGAATGTGAAT  
 GCCCTCAGAAATCACTGCTGATTTAAAAATAATCGACTTAAAACTGAAAGAAACCTTATCACAATTTTCCCC  
 AGTTCAATGCTATGCCATTACCACTCCAAATAATCTCAAAATTTTCCACTTAATAACTGTAAAGTTTTTTTC  
 TGTAAATTTAGGCAATATAGAATAATTAATTTCTGATATTGCACTTCTTATTTATATAAAATTAATCTTTAATATC  
 CAAATGAATCTGTTAAATGTTTGAATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAAGTGGTGGT  
 ATGAACAACTCTTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCAGAGCTTTCTATGTACTGTTA  
 AAATTTGAGGTACATATTTCTTTTGTATCTTGGCAAAATCTCCTGCAAGGCCAGGAAGTATATAGCAAAAAAGT  
 GAACAAAGATGAACATATGATTACATTACCATTTGCCACTGATTTTTTAAAAATGGTAAATGACCTTGTATATA  
 ATATTGCCATATCATGTGTACCTATAATGGTGATATATTTGTTTCTATGAAAATGTATTTGCTCTTGTATATAA  
 AATCTGTAAAAATGTTAGTTTGGTAAATTTTTTCTGCTGGTGATTTACATATTAATTTTTTCTGCTGGTGA  
 TAAACATTAATTAATCATGTTTCAAAAAAATAA

097855.101003

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLLEKYMDEDEGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNFYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC  
HNMNIWGQIWPKAVYLVLCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCKEKS DRY  
YPPREETNEIERQQSQVHDTHVRTRSDSSRNEVISAAQMSQIVSCEVRLRDQCKGTT CNR  
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHFIKSNRNGI  
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCP RNCMQANPHYARVIG  
TRVYDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNP PGGKAFRV  
FAVV

**Important features:**

**Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

007355.010101

## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCGCGCTCCGACGGGCGAGCGCCCTCCCCATGTTCCTTGCTCCACGCCG  
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAGAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGGTCTACGAA  
GATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCCTTCAGATGGGAGACCATCTCTCTTGTGCT  
CCAGACTTCATCAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACCTATACATCTGAGCTTTATAAGCGCCCGGA  
GGAACAATGAGCTTGGTGGACACATTTTCATTGCAGTGTTGCTCCATTCTAGCTTTGGGAAGC  
TTCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCIGTTCTCTGAGGAACTCAAGTTGGTTGCCAGAAAAATGTGCTTTCATTCCCCCT  
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTCCCAACCTGAGGATTTCTGAAAGGTTTCACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAATCAGTACTAAAGCAATATAT  
TTGTGATTCCTCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCTTTAAGAACGCCCTCCACACACTGCCCCC  
CAGTATATGCGCATTTGACTGCTGTGTTATATGCTATGTACATGTGAGAAACATTAGCAT  
TGCATGCAGGTTTCATATTCTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

09978595.101601

## FIGURE 149

MSLLPRRAPFVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

09978585.10600

# FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTGTTACCCCGGTCTCGGTCATGTTAACTCCAATGTCCTCTGTG  
 GTTAACGTCTCTGCCATCAAGTTCAACCTCATTTGACAGCCAGCACAGTATCCAGTTGTCAACACCAATTAAGG  
 CAAATTCGCGGGCTTAAGAACACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCACTTAGGGGTCCCTTA  
 TGCCTCACCCCCACTGGAGAGAGGCGGTTTCAGCCCCAGAACCCCGTCTCTCTGGACTGGCATCGGAATAC  
 TACTCAGTTTGTCTGTGTGTCGCCAGCACCTGGATGAGAGATCCTTACTGTCATGACATGCTGCCCATCTGGTT  
 TACCGCCAATTGGATATCTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCTTTACTTTAAACATCTAGT  
 GCCACGGAAGATGGAGCCACAAGAAAAACGACAGATGATATAACGAGTAATGACCGTGTGAAGACGAAGA  
 TATTCTATGATCAGAACAGTAGAAGACCCGTCATGGTCTATATCCATGGGGGATCTTTACATGGAGGGCACCGGCAA  
 CATGATTGACGGCAGCATTTTGGCAAGTACCGGAAACGTCATCGTATACCATTAACCTGCTCGGGAATACT  
 AGGGTTTAAAGTACCGGTGACACAGGACGACAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTCGGGT  
 GATTGAGGAATGTGGAGGCTTTTGGCGGGGACCCCAAGAGAGTGACCATTTTGGCTCGGGGCTGGGGCTC  
 CTGTGTGACGCTGTGTGACCTGTCCCACTACTCAGAAGGTCTCTTCAGAAAGGCCATCATTCAGAGCGGCACCGC  
 CCTGTCCAGCTGGGCGAGTGAACACACGCGGCCAAGTACACTCGGATATTGGCAGACAAGGTGGCTGCAACAT  
 GCTGGACACCAACGACATGGTGAATGCTGCGGAACAAGAACTACAAGGAGCTCATCCAGACAGCATCAACCC  
 GGCCACCTACCACATAGCCTTCGGGCGGGTGAACGAGCGAGCTCATCCAGACAGCCCCAGATCCTGATGGA  
 GCAAGGCGAGTCTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAAGGCTGAAGTCTGTGGAACGGCAT  
 CGTGGATAACGAGGACGGTGTGAGCGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
 CTACCTCGAAGGGAAGACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGACTGGGCGGATAAGGAAAAACCC  
 GGAGACGCGCGGGAACCCCTGGTGGCTCTCTTTACTGACACCAAGTGGGTGGCCCCGCGGTGGCGCGGCACT  
 GCACGCGCAGTACGGCTCCCCACCTACTTTCTATGCTCTCATCATCACTGCCAAAGCGAAATGAAGCCAGCCT  
 GGCAGATTGGGCCCCATGGTGTGATGAGGTCCCTATGTCTTCGGCATCCCATGTCGTGCCACCGAGCTCTCAG  
 TTGTAACCTTTTCAAGAAACGAGCTCATGCTCAGCGCGGTGGTTCATGACCTTTCAGACGAACTTCGCCAAACATGG  
 TGATCCAAATCAACCAAGTTCTCTCAGGATACCAAGTTCATTACACAAACCCCAACCTTTGAAGAACTGGCTG  
 GTCGAAGTATAATCCCAAGACCAAGCTCTATCTGCATATTGGCTTGAACCCAGAGTGAAGATCACTACCGGCG  
 AACGAAAGTGGCTTTCTGGTTGGAACCTGTTCTCTATTGTCACAACTTGAAGAGATATTTCAGTATGTTTAAAC  
 AACCAAAAGGTTCCCTCAACAGACATGACATCATTTCCCTATGGCACCCCGGCGATCTCCCGCCAGATATGGCC  
 AACCACAAAGCCCGCAGCACTCCTCGGCAACAATCCCAACAACCTTGAAGACCTTCAAAAACAGGGCTGA  
 GGACCAACTGCTCTCATTTGAACCAAAACGAGATTATTCACCGAATTAAAGTGTCAACCTTGGCGCTCGGCGCTC  
 GCTCTCTCTCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAAGGACAGAGGCGCCATGAGACTCACAG  
 GCGCCCCAGTCCCAGAGAAACCAACAAATGATATCGCTCAATCCAGAACGAAGAGATCATGCTCTGCGAGAT  
 GAAGCAGCTGGAACACGATCAAGAGTGTGAGTGCCTGCAGGCACACGACACACTTAGGCTCACTGCCCCGAGA  
 CTACACCTCACGCTCGCGCGGTGCGCAGATGACATCCCACTTATGACGCAACACCATCACCATGATTCAAAA  
 CACACTGAACGGGATGACGCTTTCGACACTTTTAAACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
 CGGACATTTCAACCACTAGAGTATAGCTTTGGCCCTATTTCCTTCTATCCCTCTGCGCTACCGCTCAGCAACAT  
 AGAAGAGGGAAGAAAGAGAGAGAGAGAGAAAGAGTCTCCAGACAGGAATGTTTTGTGCCACT  
 GACTTAAGACAAAAATGCAAAAAGGAGTCACTCCATCCCGCAGACCCCTTATCGTGGTGTGTTTTCCAGATTAC  
 AAGATCAACTCTGACCTGTGAAATGTGAGAGTACACTTTCTGTTAAAAATAACTGCTTTAAGATCTCAACCA  
 CTCACCTTCAATGTTTAAAGTGTAGGACATCACCATTCAAGGCCCCGGGTGTTTCAACGTCAAGGAAGCT  
 GACACTTCTGAACCTCAGCCAGGACACTTGATATTTTAAATTAACAATGGAAGTTTAAACATTTCTTTCTGTG  
 CACACAAATGATGGCTCTCTTAAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGACATGGAGCTGTAATCCAG  
 AGAGAGGAAACGTAAGAATTATTATTAAAGAAATGGAGCTGTGACGCGAAATCTGTACGGTTCTGTGCAAGAG  
 GTGTTTGGCCAGCTTGAACATATTTAAGAGACTTTGT

00078502-101601  
 100101

## **FIGURE 151**

MLNSVLLWLTALAIAKFTLIDSQLQYFVVNTNYGKIRGLRTPLEILGPVEQYLGVVPYASP  
PTGERRFQPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLEPWFTANLDTLMITYVQDQN  
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIENVGAFGGDPKR  
VTIFGSGAGACSVLLTLSSHYSGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML  
DTTDMVECLRKNKYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSNSFVDNLYGYPEGKDTLRETIKFMYYTDWADKENP  
ETRRKTLVALFTDHWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPPYV  
FGIPMIGPTLFSNCFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPKHTGPEDTTVLIETKRDYSTELSVTIAVG  
ASLLFLNILAFAALYYKDKRRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPDPYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

**Signal sequence:**

amino acids 1-24

**Transmembrane domains:**

amino acids 189-204, 675-692

U97555-20601



# FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT  
 CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
 CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAACCGGGAGCACTCGCTGTGCGAAGCC  
 TACCAGGGTGTGGGCACAGGCAGTTCCTCAGTGTGGAATCTGATGGGCAATGCCATGGTGA  
 TGACCCAGTATATCCGCTTACCCAGATATGCAAAGTAAACAGGGTGCCCTTGTGGAAACCGG  
 GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA  
 GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAGGATCGGATGCAGCCAGGGC  
 CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTGTAGACACCTACCCCAAT  
 GAGGAGAAGCAGCAAGAGCGGGTATTCCTTACATCTCAGCCATGGTGAACAACGGCTCCCT  
 CAGCTATGATCATGAGCGGGATGGGCGGCCACAGAGCTGGGAGGCTGCACAGCCATTGTGCC  
 GCAATCTTCATTACGACACCTTCCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG  
 ATGGATAATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCCCTGCC  
 CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
 TTTCTTGAAGTTGTTTGAACATGACAGTGGAGAGACCCAGAGAGGAAAAGCTCCATCGA  
 GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
 CTTGAGTGGCCTGGCCCTTCTCCTCATCGTCTTTTCTCCTGGTGTTTTCTGTATTTGCCA  
 TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCGAAGCGCTTCTACTGA  
 GCCCTCCTGCTGCCACCACCTTTTGTGACTGTCAACCATGAGGATGGAAGGAGCAGGCACGTG  
 GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGTTGGGGACTATATTCTG  
 TCACTGGAGTTTGAATGCAAGGACCCCGCATTCCTATGTTGTGTCATGGGGACATCTAACT  
 CTGGTCTGGGAAGCCACCCAGGGCAATGCTGCTGTGATGTGCCCTTTCCTGAGTCC  
 TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTACGTGGTGTGATGCCAAAATCACAGAAC  
 AGAATTTCTAGCCCAGGCTGCCGTGTGTTTGAAGTCAAGAGGCCCTTCTACTTTCAGTTTGTG  
 AATCCACAAAGAATTAAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGTT  
 TTGCATTTGACCCAAACCTCTGCCCTACCTGAGGAGCTTTCTTTGGAAACAGGATGAAAAT  
 TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCTCTCTGTGTGCAACCTGAGCTG  
 GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGGCTGCAGAAACACACCTGCGTTTTCAC  
 TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT  
 GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
 AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
 GATTAGCTGTGCAACTGACAGCTCCAGGTTTGTATCAAACCAAAGCAACATTTGTCTATGTG  
 GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCGTCATGTTTGTAGT  
 TACGATTTTGAATCCCACTTTGAGTGTGAAAGTGAAGGAAGCTTCTTCTTACACCTT  
 GGGCTTGGATATTGCCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
 TGCTGTCTCATGTTCCAAAGTCTGAGAGCAACAGACCCCTCATCTGTGCTGGAGAGGTT  
 CACTGTCTATTGAGCAGCACAGCCTGAGTGTGCTGCCCTCTGTCAACCCCTTATTCCTGCTTA  
 TTTGCAAGGGGTTACATGCTGTCTACCTTACTGCTGCTGGGATTAATCAGTTACAGGCCAG  
 AGTCTCTTGGAGGGCCTGGAAGTCTGAGTCTCTCTATGAACCTCTGTAGCCTAAATGAAAT  
 CTTTAAATCAACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTGC  
 ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCATGG

## FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911  
><subunit 1 of 1, 348 aa, 1 stop  
><MW: 39711, pI: 8.70, NX(S/T): 1  
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPGQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGGALWNRVPCFLRDWELQVHFKEHGQGKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPTLGGCTAIVRNLYDTFLVIRYVKRHLTIMDDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

### Signal sequence:

amino acids 1-38

### Transmembrane domain:

amino acids 310-329

09/05/95 10:50:10

# FIGURE 154

CCGAGCCGGGCGCGCAGCGAGCTGGGCGGGCTGGGACCATGGGCGTGAGTGCATCTACGGATCAGTCT  
CTGATGGTGGGTCGTTAACTCTCAGTGGGACTCCAAGATTTCCATGAAGAAATCAGTTGCTCTCATTCAGAAGAT  
TGGGCTCTGGCTCAGAATTCCTGCAGCTGGTGAAATCTGTTTTCTAGAGAAAGGTTTAAATTAAGCGCTGCAGTCT  
GACATGTTCCCGATTGGGTGGAACCATGAAGAGAAATAGATCTTAATAATGCTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCCTTTGTGAGCCTCAGCCTCAGCTGCTTCTCCACTGTATCCCGGTGT  
CGACTCTCAAGATGGATGAGTAGCAAGAGTGCAGAGAGAAATCATGCCGACCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCGAGTGTGGCCGAGCGCAGCATGGAGGTGATCAGCC  
CGCATCATTTTAACTGGTCTCAGTGCATGTGTTTCAATCGCCACGGAGACAGGTACCCACTGTATGTCAATCCCA  
AAACAAGCGCAGAGAAATTTGACTGCACCTCTGGTGGCTAACAGGAAACCGTATCACCCAAACTGGAGGCTTTCA  
TTAGTCACTGTCAGAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTGAACTCCTTGCCCTCTTATCCCAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGACGCAATTTGCAGAAACGGTCAGCTGGAGGATA  
TCTATCTAAAGAAACAATACTCTGCCCATTGATGGTCTGCAGACAGCTCTATTTAGAGACCATGGGAAAA  
GCCGACCCCTACAAAGTGGCTGGCTTCTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA  
GGCACCAGCCAAAGTCGCTGTTCTGCTCTGGAAGCTGCTATTTGCCCGTGAAGAAACAGTATCTGGAAGAGGAGC  
AGCGTCGTGAGTACCTCTAAGTTTGAAGAAACAGCCAGCTGGAGAAGACCTAOCGGGAGATGGCCAAAGATCGTGG  
ATGTCGCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTCTGCCCAATGTGAGCT  
TTCCTGTACAGAAATGGCTGTGTTGACTGGAGCACTTCAAGGTAAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAGACGGGAGAAAGATTTGACTTCGGGTATTTCTCTCCGGTGGCCACCCCATCTGGAACCAACCATCG  
GCCGATGCGAGCGTCCACCGAGGGCAGGAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT  
CACCAGTTCTCAGTGCTTTGGGCTTTTCAAGAGCCAGGTTCCCAAGGTTTGCAGCCAGGTGATCTTTGAGCTTT  
GGCAAGAAGAGAAAGCCAGTGAACATTCGTCGGGATTCITTAAGTGGCGTATGTCACATTCACACCTT  
CTTTCTGCCAAGACCCACAGAGCTTCTCCCAAGCCCATGTGCCGCTTGAAACCTTGGTCCGCTTTGTGAAAA  
GGGACATGTTGTAGCCCTGGGTGGCAGTGGTACAAATTAATATGATGTCATGTCAAGGAGGATCTAAAGG  
TATGAGTACAGCAGTATAGATTCATGCCAATACAGAGCATAGGGAAGGTCCACTCTAGTTTGTCTGTATC  
TAAGGGTGAAGATTAATGCTTTTAAAGGCTAAATATTTGTTTTGTTGGGAAGCCAGATGTTGGGGTTGAACAGT  
AAGCATATGCTGCAATGTGGTACGTGAATGCTGTGTAACAATAAGGCTTCAAGAGGATGAGAGGTACCT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAAATATATAGTTCAAGACCTGAAGTTGCCAATCAAGTTTGCAC  
TCTCTGGCCCTGCCATGTACTATGTGATGGAACAGCACCTCAACCAAAATTTTTTAACTCTTAGACATT  
TTTAACTCTGTTTGAAGATTTCTGAAAGTATTTATCTAAAATAAAGGTTGGCAAACTTTTCTGTGAAGG  
GCCAGATTGAATATTTTCAAGCTGTGGACCAAAAGGCCACATACAGTCTCTGTACATACTACTCAACTCTGT  
TTCGAAAGCAGGAAGCCACACAGACAGTACATAAAGGAATATGTGTAGCTGGGTCCAGGCGACAGCAAAACA  
GATGGTGACCACTTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAATAAGGCTATACATAAATTGC  
ACTCTCAGCACTTTGAGAACGAGTTGAATACCAAGAAATTAATCAATGGTTCCCTCAGTAACTCTGCTAGAAACA  
CAGAAATTTGCTCTGATCTGACACTAGAACAAAACCTTGAGGGTAAATAAATGAAATTAAGTGAATGATAGAA  
AAGTAAATGAAGAAATCTGATGTTTATGATGATTGTGGTACAGATAGTTTAAATATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATGCTGAAATTTTTGTATGCCATTTAGTATTTTATAGTTTAGGAAAAATTT  
TCTAAGACCAAGTTTATGATGACTTTATTTCTGTAGTAATATTAATTTGCTGTACCTGCTGGTGGTTAGAAG  
GAGCTAGAAGATGAATTCAGGCATTTCTTCCAATAAACTAATTAAGGCTCATTCCTTTGACAGAGCTGAGA  
ACTGGATCATTTTAAACCATTTTCTCAGTTTCAATGGTAAATTTCTGATTGATTTTAAATGCGTTTTTGA  
AGAACTTTGCTATTAGGTAGTTTACAGATCTTATAAGGTGTTTTATATATTAGAAGCAATTAATTAATCATCTG  
TGATTTCTGAACATAAGGTGCTAATTCAGAGAAATGGAAAGTGAAGTGTCTCTGTGTGATCGGCTATCC  
AATTTTTCTCTTTGTTTTGTCAGGCTTGCATTTGAATATGCTGTTTTCTATAAATAAATTTTTTAAGAAATA

09/05/95 10:16:01

## FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMDPVTEPPVTDVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNOWSADQLYLETTGKSRTLQSGLLLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF  
CQDHHKRSPPKMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

007553.10101



## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGLTWETGCTQIRYSVPPELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELVLKRALDREEKAAHHLVLTASDGGDFVRTGTARIRVMVLNDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYISLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPCENNAQITYSLAENTI  
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSLFLVDLQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIQVLADLGSLES  
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD  
GVQAFPLQTYSHVSLTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVLSYQIFFLFFNCSSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNDRYCKPPTVCL  
IYLSIYLSIYLSIYLLSCTDGS�TPVIPVLWEAEAGGSPEVGSRLPA

**Signal sequence:**

amino acids 1-30

**Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

097555-101601

## FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCAGTTAAAAG  
GCTCCAGAATCGTGTAACAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAAACCCATTGCGAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCAACCACTCCCGAGAGAATTTTCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCITACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAGGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCAAACTCT  
CTGGTTC

09976585.101601

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336  
<subunit 1 of 1, 260 aa, 1 stop  
<MW: 28048, pI: 7.87, NX(S/T): 1  
MGRPRPRAAKTWFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQLLCGGVL  
VGGNWLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIFVVQSIPHPCYNSSDVEDHNDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTDLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

0078505-107501



# FIGURE 160

GCGCGCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG  
 CGCGCCGCCACGCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCCGCGCCCCG  
 GCCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGCCCCCGCCCCCGCCCCG  
 CCCCAGCGCGGGGGGAACCGGGCGGATTCTCTCGCGCTCAAAACCACTGATCCCATAAAAAC  
 ATTCATCTCTCCCGCGCGCCGCGCTGCGAGCGCCCCGCGAGTCCGCGCGCGCGCCCTCG  
 CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGCGGGAGC  
 GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGAGCTAGCGCGCGCGCTGGA  
 TCGCGAACCGCGCGGGGAGACGGGCGCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC  
 CCGGCCAACCCCTACGATGAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
 CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
 GCCAAGGTGACGACAAGCTGCCCGCAGCGGCTGCAGGCTGTGCCCGTGGGCATCCCTG  
 CTGCCAGCCAGCGCATCTTCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
 CGTGCTGCCGCAACCTCACCATCTGTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC  
 GGCTGCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
 GGTCTGTGGACCTGCCACATTCACGGCCTGGGCGCCCTACACACGCTGCACCTGGACCGC  
 TCGCGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA  
 CCTGCAGGACAACCGCGCTGCAGGCACTGCCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
 CACACCTCTTCTGACGGCAACCGCATCTCCAGCGTGCCTGAGCGCGCCCTTCCGTGGGCTG  
 CACAGCCTCGACCGCTCTCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCGCTT  
 CCGTGACCTTGGCGCGCTCATGACACTCTATCTGTTTGCCAAACATCTATCAGCGCTGCCCA  
 CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
 TGTGACTGCCGGGCACGCCCCTCTGGGCTGGCTGCAGAGTTCCGCGGCTCCTCTCCGA  
 GGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCTCAAACGCCCTAGCTGCCAATG  
 ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGCGAGGGCCACC  
 GATGAGGAGCCGTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT  
 ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCCGCCCGGTG  
 ACAGCCCCGCGGGCAACGGCTCTGGCCACGGCAATCAATGACTCACCCCTTTGGGACTCTG  
 CCTGGCTCTGCTGAGCCCCGCTCACTGCAGTGCGCCCGAGGGCTCCGAGCCACAGGGTT  
 CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCACCCGAGCCACT  
 GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
 CTACCCAGCCTCACTGCAGCCTCACCCCCCTGGGCTGGCGCTGGTGTCTGTGGACAGTGCT  
 TGGGCCCTGCTGAGCCCCAGCGGACACAAGAGCGTGTCTCAGCAGCCAGGTGTGTGTACATAC  
 GGGGTCTCTCTCCACGCGCGCAAGCCAGCCGGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
 GTCCCTCGTATGAGCGCTGCGGCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG  
 TTCGGCGGCAGCGTTTGTTCAGAAACGCGCCTCCACCCAGATCGCGGTATATAGAGATAT  
 GCATTTTATTTTACTTGTGTAAAAATATCGGACGAGCTGGAATAAAGAGCTCTTTTCTTAA  
 AAAA

097855.104604

## FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184  
><subunit 1 of 1, 473 aa, 1 stop  
><MW: 50708, pI: 9.28, NX(S/T): 6  
MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRI  
FLHGNRISHVPAASFACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHQNRAVHVHHPAFRDLGRIMTYLYLFANNLSALPTEALAP  
LRLQYLRRLNDNPWVCDRCARPLWAWLQKFRGSSSEVPCLPQRLAGRD LKRLAANDLQGCA  
VATGPYHPITWGRATDEEPLGLPKCCQPDAAKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPFRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSEGSALPSLTCSLTPLGLALVLWTVLGPC

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Leucine zipper pattern.**

amino acids 135-156

#### **Glycosaminoglycan attachment site.**

amino acids 436-439

#### **N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

#### **VWFC domain**

amino acids 411-425



## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314  
<subunit 1 of 1, 798 aa, 1 stop  
<MW: 87552, pI: 4.84, NX(S/T): 5  
MEASGKLICRQRQVLFSLFLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLNEKLDREDLCGHTEPCVLRQVLLSPFEFFQAEQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIIISPNYSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDNDNAPEFEQPFY  
RVQISEDSPVGFLLVVKVSATDVTGTVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAFEVIMSFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTSTYTLFVRENNSPALHIRSVSATDRDSGTNAQVYISLLPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSLLFVSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGLHVDMSGTRT  
LSQSYQYEVCLAGGSGTNEPKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 685-712

#### **Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

#### **N-glycosylation site,**

amino acids 418-421, 436-439, 567-570 and 786-789

## FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCGGTAGCCGTGC  
CCGATTGCCTCTCGGCCCTGGGCAATGGTCCCGGTGCGCGTGCAGACCGCCCCGCGTCAT  
CGGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGCGCATCATATGGTGATGCTGTCTG  
TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCGAGAGAGCCTTTTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCAATTCAGCTCTT  
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCCATAATTTTATTATTTCAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC  
GAACACTGGAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAATAGGCCCTCTCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGATTTTTCTTATTCTTTTAAATAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTGGAAAAGAGGAACCTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTTAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAGRRPFRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDFPMQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFLSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAQPMARFNHTRTLETLETKIFIPNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

## **FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACG**ATG**CTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCTCTCGCCTCGCACTGCTGCTGGGCTCGGCGCGGGGCTCTTCTCTC  
TTTGCCAGCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCA<sup>À</sup>CCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGCGCTGGATCCCGCTGGTTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTGTGCTCGCTCTT<sup>CG</sup>CCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCT**A**  
**G**TCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAACATAATA  
AAATCATGAATATTTTAA

097555.0504  
100701.550266

0697-9280

><subunit 1 of 1, 295 aa, 1 stop

MLQSPGSLLLLLFLASCCCLGSARGLPLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLBQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLETIQFCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCTIPLASSDHLLPATEEAPKVEACEACKNKNDNDNDIM  
ETLCKNDLFALKI KVKEITVIINRDTKI ILETKSKTIYKLGNESEARLDKKSVLWLKDSLQCTCE  
EMNDINAPYLMVGQKGGEVLVTSVKRWKQGREFKIISRSIRKLOC

**Signal peptide:**

Cysteine rich domain, homologous to frizzled N terminus  
amino acids 6-153



## FIGURE 168

GTGGAGGCCCGGACGATGCGGGGCCGACGAGGCCGAGACGSGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACCTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTGTTGGGACCCAAACCCATTTCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCTTGTGGTTCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCCTCTGGGCGTCCCTGTGGCCAATGTGCT  
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCTATGTATCTCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCTCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA  
TGTGGACCGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGGCCTGGTGTCCAGCTGCAGGGACAGACCCTTGGCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGGA  
GTGTTCTTCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTACGCTGCATCCTGGCGGTTCTTCTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGGCACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCGGGAGCCCCCACCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCACAGCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCGTGGGTGATCACGTAAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

00970005.101501

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988  
><subunit 1 of 1, 560 aa, 1 stop  
><MW: 58427, pI: 6.86, NX(S/T): 2  
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVLYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSFVLV  
KKGEDIPLMLGVYTI PAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCFLSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GGAATGMIFVLGQAEGLIMLAMTALTVRREPSLSTCQQGEDPLDWTVSLLL MAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPTSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

# FIGURE 170

GTCCACATCTGCTCAACTGGGTGAGTCCCTCTTAGACAGGCTCTTGTCATCTTTGCTGAAGTGGAACCAAC  
TAGGTTCCCAAGTAGGGGCTCTCCCTGGCAATCTTGATCGCGGTTGGACATCTAGATCGCTTCCAATGAAAG  
TGCCCTTGCCCTTGGGGTCTGCTGTTGTTTCATAATCATCTAACTATGGGACAGAGTTGTCGCGGAGCTCTGGGG  
AAGGAGCAGGGGCTGATCAAGCATCCAGGAAACACTGGAGGACTTGTCCAGCTTTGAAAGAACTCTAGTGGTT  
TCTGATCTAGCCCTCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTTGTCAGGAGGTGACCACTCTCAGGTGAAATACCAAGTGTTCAGAGGAGTGGC  
ATCTGTTGATCAGTATCGGGAAGCTGTCTCCAGGAATCGGGGAGGAGAGGGGAGGCAAGCTTGGGGCCGCTCT  
CCAGGTGTTGTCAGCTGCTCCAGGCGCTCCCATTCAGGTGGACTCTGAGGAGAGGCTTGCTCAGCACAGGACGGCG  
GCTGGATCAGAGAGCACTGTGCGACAGTGGGATCCCTGCTGCTTCTTGTATGTCCTGCGACAGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCATGACACAGGACAGGTTTCCCAAGGCGAGCAGGA  
GCTGGGAATCTCTGAGAGCGCTCTCTGCGAACCCGATCCCTGGACAGAGCTCTTGACCCAGACACAGGCGC  
TAACACCCCTGCACACCTTACACTGTCTCCAGTGTAGCAGCTTTGCTTGGATGTCAITGTGGGCGCTGATGAGAC  
CAACATGTCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCTATTTTGTATCTGGTGTAACTGC  
CATGACAATGGGAACCCCCCAAGTCAGGTACAGCTTGGTCAAGGTCAACGCTCTTGGACTCCAATGACAATAG  
CCCTGGCTTTGCTGAGAGTTCACGTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAC  
GACCGCACACAGCCCTGACCAAGGCCCAATGGGAGAGTGGAGTTCTTCTCAGTAAACATGCTCCAGAGGT  
GCTGGCACTTTCAGTATGATGCCAAGACAGGCGAGGTCAITCTGCGTCGACCTTAGACTATGAAAAGAAACCC  
TGCTACAGAGTGTGATGTCAGGACAGGGGACCTGGGTCCTCAATCTATCCAGCCCACTGCAAGTGTCTCATCA  
GGTTCTGAGATGTCAATGACAACATCCCAAGCATCCAGCTCAATGGGCTCCAGGCATCACTGGTGTGAGAGAG  
TCTTCCCAAGGACAGTCTTATAGTCTTGTCTATGCGAGATGACTTGATTCAGGACCAATAGTGTGTGCTCACTG  
CTGGCTGAGGCAAGAGCTGGGCGCACTCAGGCTGAAAGAACTAATGGCAACACATACATGTTGTTTACCAATGC  
CACTGGACAGAGAGCTGAGCCGCAATATACCTCACTCTGTAGCCCAAGAACAGGACTCAGCCGCTTATC  
AGCCAGAAAGCAGCTCAGCATTCAGATCAGTGAACATCAACGCAATGACCTGTGTTTGGAGAAAGCAGGTATGA  
AGTCTCCACGCGGGAAGAAACACTTACCTCTCTCACTCATTACCATCAAGGCTCATGATGTCAGATCTGGGCAT  
TAATGAAAGTCTCTATCCGATCCAGCTCAGGACTCCCACTTGCTAGTACATTCAGTCACTCAACACAGAGA  
GGTCACTGCTCAGAGGTCATGAATATGAAGAGATGGCGGCTTGTAGTTCCAGGTGATCCAGAGGACAGCGG  
GCAACCCATGCTGCTCAGTGTCTGTGTGGGTGAGCTCTTGGATGCCATATGATGCCCAAGGAGTGTGT  
CCAGCTGTGCTCAGGATGGAAAGCCAGGCTCTCGTGCTTGTGATGCTTCCACAGGCGCACTCTGCTGTGGC  
CATCGAGACTCCCAATGGCTTGGGCGCAGCGGCACTACACACCTTCCACTGAGGCACTTCAGAGCTCCGCGCAAT  
CCTTTTGACCAACTTGTGGCCAGAGATGTCAGACTCGGCGCAATGAGAGCGCTTACAGCATCCGCAATAGG  
AAATGAAGCCCACTCTCTATCTTCAACCTCTATACGGGCGAGCTTGTCTCATAGTGTCAACATGTCAGAGCGCT  
CATTTGGAGTGTGATGGGAGCTGGAGATAGTATGAGAGACAGGGAAGCCCTTACAGACCCGAGGCCCTGTT  
GAGGTGTGATGTTGTCACAGTGTGGACCACTGAGGAGCTCAGCCGCAAGCTCGGGGCTTGAAGCATGTGAT  
GCTGACGCTGTATCTGCTGGCTGTATGTTTGGGATCTCTGGGTCATCTCGGTTGTATCTTGCTTGTGTCATGTCATCTGGCG  
GACAGAAAGAGAGACCAACAGGCGCTCAACTGTCTGGAGGCGCGAGTCCACTCACGCGAGCAGCCCAAGAGGCC  
CCAGAAACACATCTCAAGAGCAGATCCACCTCTGTGCTTGTCTAGGGGTCAGGACAGGTGAGCTTGTGAAT  
CGGCGAGTCCCAAAAGATGTGACAGAGGCGGATGATGGAAGCAGGCTGGGACCCCTGCTGACGCGCCCTTCC  
CCACTCCACCCGACCTGTACAGGACGCTGTCGTAATCAAGGCAACAGGAGCACCGGAGGCGCCGAGAGGT  
TGAGACAGACAGGTCAGTCACTCTCTTCAACCATCCAGGACAGGAGTATGCTCCCGGAGAACCTGAACTTCC  
CAGGCCCAGCTGTCACAGGCGGCGGCGGCTTCCAGGCTCTGAGGCTTGAAGGTCGAGGAGCCGACAGGAGCTGCG  
TGAGACAGGAGGTCAGTGGGAGGCGGCGGCTTCCAGGCTCTGAGGCTTGAAGTCTGTCGAGGCTGCTGTTGGC  
TGCTCTGCTGCGAGCGGAGCCCGCTGGAGGAGCTCACTGTGGAATCTCTCTTGTGACGAATCTCCAGCTGCT  
GTCTTGTCTGCTCAGGCGCAATTTGAGGCAATCTCAGGCCAAACCAACAGGAGAAATAGTACTTGGCCAGGACAGGAG  
CAGGAGGAGTGCATCCAGACAGATGTGGCCAAAGTGAAGGGCTGAGGCGCACAGACACAGAAACAGGAGGA  
AGGGGCTTTGGATCTTGAAGAGGAGCTCTCTGTGAAGCACTGTGAGAAGAGAGCTGTCAAGTCTGCTGAGGCC  
CAGCAGAGTCTGGCCCTGGACCGGCTGAGCGGCTGAGCCGCTGAGCCCGGCTGGATGGGCAAGACTCTTTTGGCCCTAC  
ACCAACTACGTGACAAATGTGATCTTCCCGGATGCTGACGACACGAGGAGGCGGAGGACTTCAAGACGTTCGG  
CAGGCGAGGCGCACAGGCTGAGGCCCAACAGGACAGAGGCTGGCCAGCAGCTTGTCTGGAGATGAGCTCACT  
GCTGGAGATGCTCTGGAACAGGCTCAGCATGCCCTGAGGCGGCTTCCAGGAGCTGCGGCGCTCTCTGGT  
CTGCGGAGAGCCCTCACTTTAGACTTGGCCACAGTGTGAGCCTCAGGACTGAAGTGTCAAGGGAGCCAGGTGG  
AAGAGCGGGGACTGAGGCGAAGGACAGGACAGGACAGCAGCAGCAGGAGGCTGTGATGATCATCTCAGAGCTCT  
CTGATCTCAAGAACAGGCGGCTTGGAGTCTGTGTGACAGAGTGTGTTTCAAAATCTGTGATCTCAGTACT  
CGGCGGCTGAGAACTTTAGGCTGATGCTACCTCCACAGGAGGCAAGGCCCAAGCTTCAAGCTACAGCTGAC  
TGCCCAAGAGCAGCCCTTGTGAAGCAGCTCTGATCTTTTGGAGGACAGGAGCGGTTTGTGCTGATGATAAGTGT  
TCTGGGCAAAACATATGTGGAGCAAAAGGGTCAGTCTCTGAGGACAGATGCTCCAGGAGTCTCAGGCGAG  
AAAGGGTGGCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCTGGGGGTGCCAGGAATCTCTCAGCTAT  
CAATAAAGGAAGCAGTAAAAAAGAAAAAAAAAAAAA

097555.10100

## FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLQLLLGLLPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDIVV  
GPDETKHAEILVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNNSPAPAESS  
LALBIQEDAAPGTLTKLTATDPDQGPNGEVEFFLSKHMPPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNIPIAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQD  
QGLQPLSAKKQLSIIQSDINDNAPVFEKSRYEVSTRENNLP SLHLITIKAHADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMPLASSVS VVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPGAGTDTPLATHSSRPFLTT  
IVARDADSGANGEPLYSI RNNGNEAHLFI LNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREABSTYRQPKRPQKHIIQKADIHLVPVLRGQAGEPCEVGQSHKDVDEAMMEA  
GWDPCQLQAPFHLTPTLYRTLNRNQNGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRP PASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKPGGS  
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTNTYRDNVISPDAAATEEPRTFTQFGKAEAPELSPGTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAASGMKVQGDGPGKGTGTEGKS RSGS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTACATGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACATAGGAGATCCCTTTCCCATTTCTCAGCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTCTGGATTGGTGTCTGCAACTGCCCATACACTTACATGTCTTACTTCTCT  
CAGGAATGTGACTGACACGCGATATTCTAGCCCTGGAAACGGCAGCTGCTGCAAACCATGGATA  
TGATCATAAAGCAAAAAGAAAGGATGGCAATGGCAGCGAGAACAAATGTTCCAGAAAGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAATACTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAAGCAGGCAGC  
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTGGTTACTTTTTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGTGAAGTTTGGTCCCAACACATT  
TCCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCTATTGCTCCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCAATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCCTGGTT  
TGATGTGATCTTCTGTGTCAGCGCTCTCTAGCATACTCTTCTCTATTGCTCACAAC  
AGGCACCAGAGAAGCAAATGGCACCTTTGAACTTAAGCCTACTACAGACTGTAGAGGCCAGT  
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACGAGGCCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAAGTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGCAAGACATGTCTATGGTAGCTGAGCCAAACAGT  
AGGATTTCCGTTTTAAGGTTTACATGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAAACAAAAAAGGGCGCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTATGACGTTATAATG

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGACCTGGGAGAAGG

## FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYAIRQYVVQVIFSVTFAPFSCMTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVFPFYIGYFIVSNIRLLHKQRLLEFSCLLWLTFMYFF  
WKLGDPPFILSPKHGILSIEQLISRVGVIQVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRILLQTMDMIISKIKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDPTVRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

007555-101601

## FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCNGANACTATTTTTTGGATTGGGTGGCTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

097853 10350

## FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTINTTGAATTCGGGTNNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATGTTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCAINTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTCCTC

097655-101001



# FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCTTGGGGGGCCCTCGGGGATTTGCTACCTTTT  
 TGGCTCCCTGCTCGTGGAACTGCTCTTCTCAGGGGCTGTGCGCTTCAATCTGGAGCGTGATGGGTGCTTGGCGAA  
 GGAGGGCGAGCCAGGCGCTCTTCCGCTTCTCTGTGGCCCTGCACCGGCGAGTGTGACGCCCGGACCCCGAGCTG  
 GCTGCTGTGGGTGCTCCTCCAGGCCCTGGCTCTTCTGTGGCGAGCAGGCGAATCGCACTTGGAGGCTCTTGTGCTTG  
 CCGGTGTGAGCTGTGGAGGAGTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGTCAAAAGGAAAGCAA  
 GGAGAACAGTGGTGTGGAGTCACTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACCCGATA  
 TGAGGCAAGGCGAGGAGTGGACAGAGTCTGTGGAGCGCGGATATGATTGGTGGCTGCTTTGTGCTCAGCGAGGA  
 CTTGGCCATCGGGATGAGTGGATGGTGGGGAATGGAAGTTCCTGTGAGGGAGCCGCCAAGGCCATGAACAATT  
 TGGGTTCTGCAGAGGGCAAGCTGCCGCTTCTCCCTGTATAGCCACTAOTCTCTTGGGGGCCAGGAAAC  
 CTATAATTGGAAGGGCAAGCCAGGGTGGAGCTCTGTGCAACGGGCTCAGCGGACCTGGCAACACTGGAGCAGCG  
 TCCCTACAGGGCGGGGGAGAGAAGGAGCAGGACCCCGCTCATCCGGTCCCTGCAACAGCTACTTTGGCTT  
 CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAGAGCTGAGCTTTGTGGCTGGAGCCGCCGCGCCCAACCA  
 CAAGGGTGTCTGGTCTCATCTCGCAGAGGACAGCGCCAGTGCCTGGTGCCGAGGTTATGCTGTCTGGGGAGCG  
 CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGCTGGCCAGACCTGATAGTGGG  
 TGCCCTCTACTCTTTGAGCGCAAGAGAGCTGGGGGGTGTCTGTATGTGTACTTGAACAGGGGGGTCACTG  
 GGCTGGGATCTCCCTCTCCGGCTCTCGGCTCCCTGACTCCATGTTTGGGATCAGCTGGCTGTCTCTGGGGGA  
 CCTCAACCAAGATGGCTTTCAGATATTGTCAGTGGGTGCCCTTTGATGGTGTGGGAAAGTCTTCACTACCA  
 TGGGAGAGCAGCTGGGGTGTGCGCAAACTTCAACAGTGTGAGAGGCGAGGCTGTGGGCACTCAAGAGCTCTGG  
 CTACTCTCTGTCCAGCAGCTGAGATATGATGGGAAACCAATACCTGACCTGAGTGGGGCTCCTCCGCTGACAC  
 CGAGTGTCTCTTACGGGCGAGACCACTCTCCATGTCTCCCATGAGGTCTCTATTGCTTCCAGAGACCTGAGCT  
 GGAGCAGCCCAACTGTGCTGGCGCCACTCGGTCTGTGTGGACTTAAGGCTCTGTCTCAGCTACATGTGAGTCCC  
 CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTATGATGGGCAACAGACCGGAGGCTCGGGGCGCCAGGT  
 TCCCTGTGTGACGTTCTTGAAGCCTTAACCTGGAAGAACCCAGCACAGGCTCTGGGCAACCGTGTGGCTGAAAGCA  
 CCAGCATCTGCCGAGTCTGTGGAGAGCCATGTTCCAGCTCCAGGAAATGTCAAGAACAGCTTGGGGCAATTGT  
 AGTGAATTTGCTGCTCACTGTCCAGACCCCTCGGCTCCGGCGACAGGCTCTGGGCGAGGGCTGCTGCTCAGTGGC  
 CCCCCTCTCAATGCCCAACAGCCAGCACCCAGCGGCGAGAGTCACTTCTCAGGCAAGGCTGTGGTGAAGA  
 CAAGATCGCTCAGCACTCTGCAGCTGGTTCACGCCGCTTCTGTACCGGCTGAGCGGACAGCAACGAAATTTCAACC  
 TGTGCCCATGATGTGTGATGAAGAACACAGCCCTGTTTGCATGATGGGCGAGCAGCTCATTTGGCTTGGAGCTCA  
 GGTCACTGCTGCCATGCCAGCCAGCCAGCCAGGCTGATGGGATGATGCCATGAGAGCCAGCTCCTGAT  
 TGGCTTTCTGATCTCATCTGCACTACTCAGGGGTCTGGGCGCTGGACCTGCGGAGAACCACTTGTGCTGTCCAA  
 TGAGATGCTCTCCATGTTTGAAGTGTGGGAGAACCCATGAAGAGAGTGCACAGTCACTTCTACTCTCAT  
 CTTTTCAGCACTCCGGATCAGCACTGAGACCAAGGAACTGGAGGTGAGAGTGTCTGTGGCAAGATCAGTGAGCA  
 GGAGCTCATCTCAGTCTCTGCAGAGCCCGTGTCTTCACTGAGCTGCCACTGTCCATGTGAGGAATGGCCATTTCC  
 CCAGCAACTCTTGTCTCTGGTGTGGTGGGGGCGAGAGGCCATGCACTGTGAGCGGGATGTGGCGAGCAAGGT  
 CAGATGATGGGTCACTGTTTCAACCAAGGCAAGTCTCAGAACCCCTGGCTGTGCTTCTTCAACTCATGTG  
 GCCTCATGAGATGTCCAAATGGGAAGTGTGTGCTGTACCAATGCAAGGTGTGAGCTGGAGGGCGGGCAGGGGCTGG  
 GCAGAAAGGCTTTGCTCTCCAGGCCCAACATCTCTCACCTGGATGTGGACAGTAGAGGATAGGAGGCGGCGGGA  
 GCTGGAGCACTGTGAGCAGCAGGAGCTGTGAGCGGAGGAGCCAGCACTGTCTGGTGGCCAGTGTCTCTGTC  
 TGAGAGAGAGAAAAACATCACTTGGATCTGCGCCCGGGGCAAGGCAACTGTGTGGTGTTCAGCTGCCCACTCTA  
 CAGCTTTGACCGCGCGGCTGTGCTCATGTCTGGGGCGCTCTCTGGAACAGCACTTCTGTGGAGGAGTATCTCAGC  
 TGTGAAGTCCCTGGAAGTGAATTTGCTCGGGCCAACTACAGTGAAGTCTCTCAATAAGAACTGTGATGCTCCGAGA  
 TGCTCTCAGAGTGTCCAGTGTGATATCTGTGACCCCATGGCTGTGGTGGCAGAGGAGTGGCTGTGTGGT  
 CATCTCTCTGTGTGATGTGGTGGGCTGTGTGTCTAGCACTGTGTGTGTGTCTCTGTGGGAGATGGGATTTCTT  
 CAAACGGGGGAGCCTCCGAGGCGCACTGGTCCCTAGTACCATGCGGTGAAGATTCTCTGGGAGAACCCGACAGCA  
 GTTTCAGGAGAGGAGAGCGGCAACCTCTGAGGAAACACTGGGGCAGCCCCCGGCGGGAGGGCCCGGATGCAACA  
 CCCCATCTGGCTGTGCTGACGGGCTCCGAGCTGGGCGCCGATGGGCTCAAGGGCAGGACCCCGCTAGTGTTC  
 GAGTCTCCAGCTGGCTGTGGCTGCCCTCCATCCCTTCCCAAGAGATGGCTCTTGGGATGAAGAGGATGAGAT  
 CCGTGTGTGTGTGCTCAAGATTGGCAGGATCGGCTTCTCAGGGGCAAGGATCTTCCACCCCAAGAAC  
 TCCTTCCACCCAACTCTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGGACAGGCGCATGGGTTAGGG  
 TGAGAAAGGGCAGGGGTGTCTGATGCAAAAGTGGGGAGAGGAGTCCATACTCCCTTCTCCCTTCACTGTGT  
 GTAACAGGAGCCAGGACCTGCTCCCTCCCGGAAGTGCCTTAACTAGAGGCTCAGGAGAGGATGTGTGCTACTGA  
 CTCAGGCTGCTCTTCTGTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCACTGAGTGGTTTGTGGT  
 TCTGCTATTATTAAAAAATATTGTGAGAACAAAAAATAAAAAA

00978585-101601

## **FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALAPGQANRTGGFLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGGGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDLDGGGEWKFCBG  
RPQGEHQFGFCQCGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSFGFYS LAVADLNSDGPDLIVGAPYFFERQELGGAVVYVLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLNQDGFDPDIAVGAPFDGDGKVFYIHGSSSLGVVAKPSQVLE  
GEAVGIKSPFGYSLSGSLDMDGNQYPDLLVGSGLADTAFLFRARPIHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLADTDRLRGQVPRVTFLSRNLEBP  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGGQLPPVAP  
ILNAHQPSPTQRAHIFHLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFFYLILSTSGISIEETTELEVELLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFGSGVVRGERAMQSERDVGSKVKYEVTVSNQGSRLTGLSAFLNIM  
WPHEIANGKWLLYPMQVLEGGQPGQKGLCSFRPNILHLDVDSDRRRRRELEPPQEPEGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLPYSFDRAAVLHVWGLRWNSTFLEBY  
SAVKSLEIVIRANITVKSSIKNLMRLDASTVIPVMVYLDPMAVVAEGVPWWVILLAVLAGLL  
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIIPREDRQQFKKEKTGTILRNNWGSPPRREGP  
DAHPILAADGHPHGLPDGHPGPGTA

### **Important features:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 1040-1062

#### **N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### **Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

**FIGURE 178**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACACAAGATGCTCAAGGTGTCAGCCGTA CTGTGTGTGTGCAGCCGCTTGCTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGGCGGTGGCTGCAGCCGGGGGGCGGTGCGACGGCGGTAATTTTC  
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGAGTCCAGGAAAACCCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGCACATTGC  
CCATGTCTTCAGATAAGCCCAAGCAGTACAAGCAGAAATGTGAAGAGCATGCAGTGACCT  
GGAGTTCAAGGAAGTGGCAACAGATTGCGGGACTGGTTCAGGCGCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCTGAGAGAAGCAGATTGCATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCACTCAGAGCTCAGAAGCATTACCTTGATAAGAAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACAATGTGTCAGTGTGACAGTGTGCTGCTGTGTTGACAGATATGGAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATGAAGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTAAAAATATCTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTGTATAATTATTTGAAAAATTCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGCTCA  
GTCAGACAAAAATAAGTTTTGAGTGTACTATAATAAATTTTTCACGAGAACAAACTTTGT  
AAATCTCCATAAGCAAAATGACAGCTAGTGTGCGGATCGTACATGTTAATTTTTTTGAAAG  
ATAATCTAAGTGAATTTAAAAATAAATAAATTTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGTGCAGCAGCTCCAGA

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829  
><subunit 1 of 1, 436 aa, 1 stop  
><MW: 49429, pI: 4.80, NX(S/T): 0  
MLKVSAVLCVCAAWCQSLSAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRPERSRFDTSLPI  
CKDSLGMFNRDLDTNYDLLDQSELRSIYLDKNEQCTKAFNNSCDTYKDSLISNEWCYCFQ  
RQDPQPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGYKPTQCHGSVGQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

0978555.101501



## **FIGURE 181**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKRSRT
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

## FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTCTGGATG  
CTGCTTTCTCTGCCTCATTTCTCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACACAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCTTGAAGAGAATATTTCTCCCCAACTGCCCTACCTGACTACCTTGTCTATGATCCTCC  
TTCTTTTTCTTTTCTTCACTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

00970505.101601

## FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965  
<subunit 1 of 1, 175 aa, 1 stop  
<MW: 19330, pI: 7.25, NX(S/T): 1  
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIWGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **C-type lectin domain signature.**

amino acids 146-171

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## **FIGURE 184**

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC  
TGCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

0997853 101601

## **FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCATGTATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAAATCTGTCTGCGCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGATGGGTATTCAGAAGAACCACCTTGTCCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTGTGCTA  
GACACTTCTGTTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGTCTGTCT  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTTCTTAGGCTTCACTTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGAAGAGCTTTGTTTCTTTATGAACTCCCTGT  
TGATTGCAGTAAATTAAGTATTTGTAATTTCTAGTGTGGCACTTACCTGTAATGCAATGA  
AATTTTAATTTATTTTCTAAAGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTTGAAGTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAGCATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAAGCGA  
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGACTATCTTAATGCTTAAATATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAAAAAAAAAA

## FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIDNYQPYPCAEDDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKFVLKEGQVCTKHRRKKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 256-259

#### **Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

097551-10101

## FIGURE 188

TGTGTTTCCCTGCAGTCAGAAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCAC TGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

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# FIGURE 189

GAGGAACTACCGGTACCGGCCGCGCTGGTAGTCGCGCGGTGGTGCACCTCACCAATCCCGTGGCGCGCGG  
 CTGGGCGGTGGAGAGTGGGTGTGCTCTCTCTCGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTTCGCGCGCA  
 GGGTTTGGAGATGGGGGAGTAGCTTACAGGAAGCGACCCGCGATGGCAAGGTATTTTTTGGTGGAAATGAAAGGA  
 AGTATTAGAAATGAGCTGGAAGCACTTACAGATTAAATATTTTGGGCAAGATCTTGGTAGCTTGATCACTCCCT  
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATACATCAACTGGAACCGAGTGAATCTTAAATGTTTCA  
 TTAATCAGAATCTGCATAAGAAAGAAATGGAGTCTGGTTAAATAAGATGACATATACAGAGCTTGAAGAAG  
 GATCATTTCTCTGTTTTCTGTAGTGTATATGGCCATTTTGTGGGACAGATCAGGATTTTACAGTTTACTCTGG  
 AGTGTCAAACACTCGCAAGCAGTAGAGAAATAAGCAAGCTTTCAAGAAATTTGGCATTGGAATACATCTCTGATTA  
 AAACCCGAATACCCCAAATGTCATGTGGCATTTTTTTAAAAATAAATAGAGCATATTGAAGTACTCAAAGATGAAGA  
 CTCTACGGAAGAAATGTAGCAAAATATGGAGAAAGGGACTTGGAGTAATCAAGGTGGCCAGTATGAAGCTGGAA  
 TCTATTATCTGTTAGATTTTTGGTATTTATGATGATGATCTCGAAATCATAACTTGGAAAGAGAGAAATTTGATGC  
 TGCTGTTAAATCTGGAGAACTGTGGTTTGTAAATTTTACTCCCGAGGTGTTTCACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTACTTTCGAATTTGGAGCTGTTAACTGTGGTGATGATAGAA  
 GCTTTGGCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTCGGTCTGGAATGGCCCCAGTGAATA  
 TCATGGAGACAGATCAAAGGAGATTAGTGAAGTTTTCGAATGAGCATGTAGAAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCACTCCATCAAACTGCTTTTGTCTGGTATTTGGCTGGGTGATCACTTTTGTTCAA  
 AGGAGAGATGTTTGTACTCACAAGACAGCTCAGGCTTGTGGCATGTTGTTTCTCAACTCATTTGATGCTAA  
 AGAAATATATTTGGAAGTAAATACATATCTCCAGATTTTGAATCTTTCGGCAACACACTAGAGGATCGTTT  
 GGCTCATCATCGGTGGCTGTTATTTTTCATTTTGGAAAAAATGAAATTAATGATCTGAGCTGAAAAAACT  
 AAAAACTCTACTTAAAAATGATCATATTTCAAGTTGGCAGGTTTGAATGTTCTCTGACACAGACATCTGTAGTAA  
 TCTGTATGTTTTCAGCGCTCTCTAGCAGTATTTAAAGGAACAAGGAACCAAGAAATGAAATTTATCATGGAAGA  
 GAAGATTCTATATGATATATCTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCAAGCTTGGACCTTCAA  
 TTTTCTCCGAATGACAAGAACACTGGCTTGTGATTTCTTGGCCCCCTGGGTGTCACCATGTGCAGCTTTACT  
 ACCAGAGTACGAAGAGCATCAATCTCTTTATGTTGAGTCTTGAATTTGGTATCACTAGATTTGACAGTTTATGA  
 GGGAGCTCTGTAAGTATATAAATCTCAGGCTTATCCAAACAAGAGTGTATTCACAGCTCCAACCTCATGAGTA  
 TGAAGGACATCATCTCTGCTGAGCAAAATCTTGGAGTTCTAGAGGATCTTATGAATCTCTCAGTGGTCTCCCTTAC  
 ACCCCACCTTCAACGAATGATTTACACAAGAAAAACAACGAAGTCTGGATGGTTGTTTCTATCTCCGTG  
 GTGTCATCTTGGCCAACTTTAATGGCAAGATGGAAAGAAATGGCCCGGACATTAATCTGACATGATCAAGCTGGG  
 CAGTATAGATTTGGCAACAGTATCACTTTTGTGCGCCAGGAAACAGCTTCAAAGATAGGCTTGGATATAGATTTT  
 TCCCCAAAAATCAAATAAAGCTTATCAGTATCAGAGTACAATGCTGGGAATAGGGAATGCTTATCTCTGAGAAT  
 CTGGGTTCTAGATTTTACTCTAGTATCCACAGATCAACACCTCAGACTTTCACTGAAAAAGTCTCTACAGG  
 GAAAAATCATTTGGGTGATGTTTATGCTCTCTGGTGTGAGCTTGGCAGAAATTTGCTCAGAAATTTGAGCT  
 CTGGCTAGGATGATTAAGAGAAAGTGAAGCTGGAAAGTAGACTGTGAGGCTTATGCTCAGACATGGCCAGAA  
 AGCTGGGATCAGGCGCTATCCACTGTTAAAGTTTATTTCTAGAAAGAGCAAGAGAAATTTCAAGAAAGACA  
 GATAAATACAGAGATGCAAGCAATCGCTGCCCTTAATAAGTGAAGAAATTTGGAAGCTCTCCGAAATCAAGGCAA  
 GAGGAATAGAGATGAACCTTTGAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGTACATCAG  
 AAGACACCTATTTAGAAATGTACATTTATGATGGGAATGAATGAACATTATCTAGACTTGCAGTTGTACTGCCA  
 GAATATCTACAGCACTGGTGTGAAAGAGGGTCTGCAAACTTTTCTGTAAGGGCGGTTTATAAATATTTTA  
 GACTTCTCAGGCTATAATATATGTTTCAACATGAGAAACAAGAAATAGAGTCAATCATGATCTCTTGTATTTGCT  
 TTTTAAACCTTTTAAAAAATATTAAGACGATTCTTGTGTCAGAGCCATACAAAAGTGGCTGGATTCAGTCAATG  
 GACCATAGATTTGCTGCCCTCGACGGACTTATAATGTTTTCAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAGTGTCTAAGTTGTATAAAGTCCACTTCCCTTCACTGTTTGGCTGACCTGAAAGAGGTAATCT  
 TAGTTTTTGGTCACTTGTCTCTCAAATGCTATCCCTAACCATATTTATATTTGTTTAAAAACACCCAT  
 GATGTGGCAGAGTAAACAAACCTGTTATGCTGTATTAATATGAGGATGTTCTCATTTGTTCTTCTCTCTCA  
 AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGATATATGTCACACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAATCTGAGGGAAAAAATTA  
 TAGCAATTAACCTGGGCACTGTAGAGATCTCCTAAATATGTTATCAAGTATTTAGATTTCTATATTTAAAGATATA  
 TGTGTTCATGTATTTTCTGAATGCTTTTATGATAAATTTCCCACTGATAGTTGATTTTGGGCACTTAATAT  
 TTACATATTTGCCCTCTGAACTTTGTTTGTACCTGATCCTTTTATTTACATTTGGGTTTTCTTTCTATGTTTGG  
 TTTTTTCACTGTCGCACTTATTTTATTTATTTCAAATAGGAAAAATTTTACAGTTGTTTACTGTAGCTTAT  
 AATGATACTCTAGTTATTTCAAGTTTACTAGTTTACTGTGACAGGGCTGCCCTTTTCTAGTAAATATTTGACATAATA  
 ACTGAAGTATTTTATAGAAAACTCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA  
 CTCAAAGAAATCACAAATTTGTGAGTAAATGATGTTGTTAGTTATATAATTCAGAGTGTACAGAAATGTTAAAAAT  
 CCAATCAGTCAAAGAGGTCAGTGAATTAAGGCTTGCACCTTTTCAAAAAAAAAAAAAA

00713636.101601  
 101601.00713636

## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439  
<subunit 1 of 1, 747 aa, 1 stop  
<MW: 86127, pI: 7.46, NX(S/T): 2  
MGVWLNKDDYIQRDLKRIILCFILIVYMAILVGTDAQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNPNNAHGDFLKLINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYSEWNYRYDFGI  
YDDPEIITLERREFDAAVNSGELWVFVYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDERSKESLVSFAMQHVRSVTTELWTGNFVNS  
IQTAFAAGIGWLITFCCKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVVIHNLPDFELLSAN  
TLEDRLAHHRWLLFFHFCKNNSNDPELKKLKTLLKNDHTQVGRFDCSSAPDICSNLVVFQF  
SLAVFKGQGTKEYEIHGHKKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSNIEYEGHHS  
AEQILEFIEDLMNPVSVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGVKAGKVDC  
QAYAQTCCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGRNKDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

AGACAGTACCTCCTCCTAGGACTACACAAGGACTGAACCAGAGAAGGAGGACAGAGCAAA  
GCCATGAAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAA  
GTCGTTGGTGAAGTTTTTTCATTCTCAGAGGAGAAAACTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGC CGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAAATCATG  
GCCACATCGTACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTTACCTCATCCCATAT  
TGTTCACGCAAAATTTGCCGCTGTTGGCTTTACAGAGGCTGTGACATCAGAACCTCAGGCCCTT  
GGGAAAACTGGTATCAAAAACCTCATGCTCTCGCCAGCTTTTTGTGAATATCTGGGTTACCA  
AAAATCCAAGCAAGAATTTATGGCTGTATTTGGAGACAGATGAAGTCTGAAGAAGTCTGATA  
GATGGAATACTTTACCAATAAGAAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTTCTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTC AAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAAGCTTTATTTACATATTTT  
TCAGTCTGTATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTCTTCTCAAGAATATTTACGTAGTTTTTTCATAGGCTGTTTTTCTCTT  
TCATGCCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAGGTTTTTCTTTAAGATAT  
TTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGGAACT  
TATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTC AATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTTAAGATTTCAGCATTGAAAGATTTCCTTAGCCTCTTCCTTTT  
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTTCTAGCCCCATGA  
TAACCTTTTCTTTGTAATTTATGCTTTCATATATCTTGGTCCAGAGATGTTTAGACAAAT  
TTTTAGGCTCAAAAATTAAGGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA  
CAATGGACCCCAAGAGAGAAA



## **FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIIIEILLILLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAABCRKLGVTAHAYVVDSCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHI VTVASVCGHEGIPYLPYPC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPV FVNTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

## **FIGURE 193**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG  
ATGCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGTGGGGTCGGTGTTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCTCTCT  
CTAGGCCGCACACGGGGCCCGCGCTGCCACGCCCGGGCCGGACAGGGACAGGGAGCTCAG  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGTGCACCGGGTGCGCCCTACCGGACCCGCTGCGCATCCGCGCGAGCA  
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCTGTCGCGGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCGAGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTGCGCGTGCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCCGCCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCGAAAACCTCTCTC  
GAGACTGAAGCTTTCGCGTTGCTTTTCTGCGGTGCCTGGAACCTGACGACACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTAAAGATTAATATATTTCAGGTATTTAATACGA

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSFMILLIIIVYWDSAGAAHFYLHTSF SRPHTGPPPLPTPGPDRDRELT  
DSDVDEFLDKFLSAGVKQSDLPKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFFTKEAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMI VLS  
GSLLRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKYYTKFLFVRDPF  
VRLISAFRSKFELENE EFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAQQLLQLQVDRQLRFPPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD

**Important features:**

**Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

## **FIGURE 195**

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTACTCAGGAAGATGATG  
TGAAGACCCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCAACCCACCCACAGAGGCCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA  
AGAGTCAAGGAATGTCATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAAACATCTGGACCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGTGGCCAG  
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCCTGGCCTCCGA  
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCGATATCCCTTCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

## **FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFRGLDCVNNAGHHPPQRPPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTFPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

0978557-101601

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGACAGCTTGGCGGAATGACTGGCCTCACAACTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA  
CCATCCTCCTTGACACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

097552 101501

## **FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEBY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCL  
GCVNPFMTQEDRSMVSVPVFSQVFPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

# FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCTTTGAAAAACCCGCGGG  
 CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCGCCGAGAACCCCTCGCTCG  
 GCGCCCAACATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
 CGCGGCTGTGGCGGGCAGCGGCGAGCCCCGAGGAGGCGCGCTGCCGCGGAGCAGAGCCGGG  
 TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
 TACGCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAGATGGGAGGCTTTTGCAAGAA  
 TGGTGAAATACCTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAGAACCCAGGTTTGAGTG  
 GCGGCTTCTTTGTCAACACTCTCCAGCATTTTTTCATGCAAAAGGATGGGATATTCCCGCGT  
 TATCGTGGCCAGGAATCTTCAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
 AGTCGAGCCTCTGACTGGCTGGAATCCCGAGCTTCTTAACGATGCTGGAATGGCTGGCT  
 TTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT  
 CCTGCTTGGTGTCTTATGTGTTTTCTGTCATAGCCACCTTGGTTTTTGCCCTTTTATGGG  
 TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTATCTGAGC  
 GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
 GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGATAGATGATGAAGAAGA  
 GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGCGTG  
 CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
 ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCGAGC  
 TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
 TGTAGATTAAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCTTTGG  
 CCTGCACTTTGTACCAAACTCTTAATTTTTCTGATGAGCAAGCTTCTTTAAAGATGCT  
 CTCAGTCAATTTGGTCTCATGGCAGTAAGCCTCATGTATATACTAAGGAGAGCTTCCAGGTGT  
 GACAAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGAGAGACTGGGATGGGAA  
 CAAGTTCATTTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCTCTAATC  
 AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAATGAAGCCAAGCAGGAGCCTTGGCT  
 CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCTCTTTCTTGTGTAAAGTATTTAT  
 TTTTGTCAAATTGCAAGAAACATCAGGCACCAAGTCAGTGATGAAAAATCTTTACAGCTAGAA  
 ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCTGT  
 TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCACCATTGGGCATTGAGGCTCT  
 CCACACTCTTCACTATTATCTCTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
 TGTGTTTTGTTCACTTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
 GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
 TTACAAGACAGATTAATAAAAAAATGTTTTGTCCAAATATAGTGTGTTGTTGATTTTTTTTT  
 AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAGGATGCT  
 CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCACTCAAGGGGTTCCCTGGGCTTTGAAC  
 TACTTTAATAATACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAA  
 GAATTAATGAACCTCCAGTACTGAAAGTGAAGAGATTGATTTTTGTTTCCATCTTCTGTAATC  
 TTCCAAGAATTATATCTTTGTAATCTCTCAATCTCAATCTACTGTAAGTACCAGGGGAG  
 GCTAATTTCTTT

00073575.101001



## **FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433  
<subunit 1 of 1, 349 aa, 1 stop  
<MW: 38952, pI: 4.34, NX(S/T): 1  
MAGGRCGPQLTALLAAWIAAATAAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQTDSWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEAEAEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

09/05/2013 11:01 AM

ATCTGGTTGAAC TACTTAAAGTTAATTTGTTAAACTCCGGTAAAGTACCTAGCCACATGATT  
TGACTCAGAGATTCTCTCTGTTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAGAGCTCC  
CAAAATGCTATATCTATTTACGGGGCTCTCAGAAACAATGGAATATCTCCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACCTCAATTACACTTCGACTCTCAAGACCAATACAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCTCTTGGCGCTCATTTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTCGGTACCATGGGGGTTCTTTCC  
AGCCGTTCTCTCTCCTAATTGGGATTATATAGAGAGAGCTGTTATCTATTACAGCATGCTAC  
AAATTCCTGGGATGGGAAGTAAAGACAATGCTGGCACTGGGGCTCTAATCTCTAAAGATA  
ACAGCTCAAAATGAATTGGGATTTATAGTAAACAAGTGTCTCCCAACCTGATAATTCAITT  
TGGATAGGCGTTTCTCGGCCCCAGTACGTAGGATACCTGGCTCTGGGAGATGGATCAAACTT  
CTCTCTCTAACTTATTTAGATCAGAACCACAGCTACCAAGAAAACCCATCTCTCAAAATTTGT  
TAGGATTAACCTGTGCAGTCAATTTATGACCAAGCTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAGAAGCTGTTCAATGCTAAGAGGAAGGCTGGAGAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGTACAGAAAAGAGTTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGTCACTTTGGCCAACTGTAAATCTTAACCAAGAAATTAAGGAGGAGAGCTGTGATTCTT  
GTATTTGTGCACCTACAGGTAGGCTAGTATATTTTCTAGTAGTAGATCCTGAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCATGCACTATCTCTCGC  
CTACGCCCTCAAGTAGCTGGGATTCAGGTGCATGCCACATGCAGGCGTATTTTGGTG  
TTTTTTGTAGAGACTTGGGTTTTGCGATGTTGACCAAGCTGGTCTCTAACTCTCGGCTTAAG  
TGATCTCGCCGCTCTGGCCTCCCAAGTGTCTGGGATTACAGATGTGAGCCACCAACCTGG  
CCCAAGCTTGAAATTTTCACTTGCCATTGACTTGGCAATTACCTTGGGTAGCCATAAGCGA  
ATGTTTAACTTTGGCTCTCATCAGAGTTGTTTCACTGCTCAACCAATGCCATTGAAGTGCAGCGT  
GTGTTGCCACGATTTGACCTCAACTCTAGCAGTATTCAGTTATGAATGAGGTGGAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTTATTTTCATCAGTATGATCATAACTTATGATTATCATCTTAGTAAAAAGCAGGAATCCTTA  
CTTTTTCTTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAACTCTT  
TTTTTTTTTTTTTTTTTTTGAGACAGGCTTCGCTCTTGTGCCACGGCTGGAGTGCAGCG  
CAGGATCTCGGCTCACGCCAACCTCGGCCCTTGGGTTCAAGCAATTCCTGCTCAGCGT  
CCCAAGTAGCTGGGATTACAGTACAGGCACCACCAACCCGGCTAATTTTGTATTTTTTGT  
AGAGACAGGGTTTCTCATGTTCGGTCAAGGTAGTCCCAAGCTCTGACCTCAAGTATCTGC  
CTGCCCTCGCCTCCCAAGTGTCTGGGATACAGGGCTGAGCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGAAACTGCTCTCATAGGAAAGTTTCTGCTTTTTTAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATGAAGAAAGTAACCAACCTATTGGA  
ACAAGTATTAACAAATTTGGAATATGTTTTATTTAGTTTTGGTATGACTGTTTACAAATCTT  
ACCAATTTTTTTCAGTAATATCTGTAATAATGGTATTTAGGAATGAACATATTTTCTCATG  
TGCTGATTTGTCTAATTTTTCATACCTTTCCCACTGGTGCTATTTTATTTTCCAATGGATA  
TTTCTGTAATTAAGGAGGCATTACAGTCTCTCTAATGTTGATTAATATGTGAAAAGAAAT  
TGTCAAAATTTTACTAAATATGCGATTTAAAAATGGATGATTTATGTTATGTGGGATTTCAAT  
TTGCAAAAAAAAACCTCTTATCAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

## FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912  
<subunit 1 of 1, 201 aa, 1 stop  
<MW: 22563, pI: 4.87, NX(S/T): 1  
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

09978555-101501

# FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGGAGGACCTGCCAGACTGGAGGGTCTCGCTCTGTCA  
 CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACTCCGGGTCTCAAGTGATTTCTCATGCG  
 TCAGCTCCCGAGTAGTGTGGGATTACAGGTGGTGACTTCCAAAGATGACTCCGTCCGAGGAAAATGACTCCCCAG  
 TCGCTGTCTGCAGACACACTGTTCTCTGTGAGTCTGCTCTTCTGGTCCAAGGTGCCACCGCAGGGGGCCACAG  
 GAAAGCTTTCCGTTCTGCAGCCAGCGGAAACAGACACACAGAGAGCAGCTCCATCAACAAACACACAGAGACTTG  
 CGCATCTCCATCGAATCTCGAAGAGGCCCTCAGAGTCATGCCCTTTCCCTGCAGCCACCCCTGCTTCCCGA  
 TCCTTCCCTGACCCAGGGGCCCTTACCACTTCTGCCTTACTGGAACCGACATGCTGGGAGATTACATCTTTCTC  
 TATGGCAAGCGTGAATCTTGTCTGAGTGACAAAGCCCTTAGCCTCTCTGCTTCCAGACACAGGAGGAGAGCGTGC  
 CTAGGGGCCCCCGGTGTAGCCACTTCTGTCACTCTCTGGTGGAGCCCTCAGAACTCAGCCTGCCAGTGTCCAGTGC  
 GCCAGCTTCACTTCTCTCTTCCACAGTCTCTCCACACAGGCCCTCACAATGCCCTGGTGAGCATGTGGAGGCTC  
 AAAAGGGACCTCCAGTGTCTCAGCCAGTTCCTGAAGCATCCCAAGAGGCCCTCAAGGAGGCCCTCGGTGACCCCC  
 GCCAGCCAGCAGTTGCAGAGCCTGGAGTGAAGTGAACCTCTGTGAGATTCTAGGGGAGCATGGTGTCTCTCGAG  
 GAGGACCCGATCAACGCCACCGGTGTGAAGCTCCAGCCCAACAGCCGCCCTCCAGACCTGCATCACTCCCTCCGG  
 CAGGAGGAGGAGCAGAGCCAGATCATGGAGTACTCGGTGCTGTGCTCCGAACTCTTCCAGAGGACGAAAGGCC  
 CGGAGCGGGGAGGCTGAGAGAGACTCTCTCTGGTGGACTTCAGACGCCAAGCCCTGTTCCAGGACAAAGAAATTC  
 AGCCAACTCTCGGTGTGAAGGTCTTGGGATTTGTGGTACAGAAACCCAAAGTAGCCAACTCAGGAGGCCCGGTG  
 GTGCTCACTTTCAGACCCAGTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTGAAGACCCACA  
 TTGAGCAGCCCGGGGACTTGGAGCAGTGTCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACACTCTGCTTCTGC  
 AACCACTTGACCTACTTTGCACTGCTGATGGTCTCTCGGTGGAGTGGACGCCCTGCAGACAGCACTGACTGAGC  
 CTCCTCTCTACGTGGGCTGTGTGCTCTCTGCCCTGGCCTGCTTGTCAACATTCGCCCTCACTCTGTCTCCAGG  
 GTGCCCTCGCTGCAGGAGAAACCTCGGACTACACCATCAAGGCTCAAGGCTCGCTGCTGAGCACTGCTGCTCTTC  
 CTGCTGGACACAGCTTCTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCAGCCAGTGGC  
 ATCTTCTGCACTTCTCCTGCTCACTGCTCTTCTCTGGATGGGCTCGAGGGCTCAACACTCTACCGACTCGTG  
 GTGGAGGTCTTTGGCACTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCATCTTCT  
 CTGGTGACGCTGGTGGCCGTGGTGGATGGAGTGGACAATGAGCCCATCATCTTGGCTGTGATAGGACTCAGAG  
 GGCCTCATCTACCTTCCATGTGCTGGATCCGGGACTCTCTGTGCTAGCTACATCAACAACTGGGCTCTTCACTC  
 CTGGTGTCTTCTGTTCAACATGGCCTGCTAGCCACCATGGTGGTGAGCATCTGCGCGCCGCCCAACACCCAA  
 AAGTGGTCACTGCTGTGACACTGTGGGCTCAGCCTGTGCTCTTGGCTGGCTGGGCTTGTATCTTCTCTCC  
 TTTGCTTCTGGCACTGCTCACTGTGCTGCTCTTACTCTTTTCACTCATCACTCTCTTCCAGGCTTCTCTCATC  
 TTCATCTGTGACTGGTCCATGGGCTGCAGGCCCGGGTGGCCCTTCCCTCTGAAGAGCACTCATCAGCCAGGCC  
 AGGCTCCCATCACTGCTCGGCAGCACTCTGCTCAGCCGCACTCTAGGCTCAGCCGCACTCTGCCATGTGATGAAG  
 CAGAGATGGCGCTCTGTCCACACTGCTGTGGCCCTCCGAGCCAGGCCAGGCCAGTCAAGCCGAGACT  
 TTGGAAGCCCAACAGCACTGTGAGAGATGGGCCCTTGGCATGGTGGAGCGACTCCCGGGCTGGGCTTTGAATTG  
 GCCTTGGGAGTACTTGGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGGCGCGCATGCTGCTCGTAGGGTACTG  
 TCCCACATCTGTCCCAACCCAGCTGGAGGCTGGTCTCTCTTACAACCCCTGGGCGCAGCCCTCATTTGGTGGG  
 GGCAGGCTTGTGATCTTGGAGGTCTGGACATCTTAATCTGTGCCCTGGCTGGGAGAGAAATGTGGGCTCA  
 GTGCTCTCTGCTCTGCTGCTCACTCTGAGGCACTCTGATCTCTGTCAATTTAACTCAGTGGGACCCAGG  
 CGAATGGGCGTCACTCAGCACTTCAAGGCCAGAGCCCTGGCGAGGAGAGGCCCTTTCAGGAGACACAGCAGC  
 AGCTCGCTCACTCTGAGCCAGGCCGCCCTTCCCTCTTCCAGCCCCAGTCTCTCCATCTTCTCTGGGTTCT  
 TCTCTCTTCCAGGGGCTCTTGTCTCTCTGTTACAGCTGGGGGTCCCGATTCCAATCTGTTTCTTGGGGA  
 GTGTTTCCAGGAGTGGCTGGTGTCTGTGCTGAATGTTTGTCTACTGCACAAGCTCTGGGCTGCCCTGAGGCA  
 GCTCGGTACCGATGGTGGGCTGGGCTAGGCTAGGCTCTGTCATCTGGGCTTTGTATGAGCTGCATGAGCCTTG  
 CTCACTCTGACCAAGCAGCACTCTCAGAGGGGCCCTCAGCCTCTCTGAGGCCCTCTTGTGGCAAGAACTGTGGA  
 CCGTGGCAAGTCCGTCTGTTTCTCATCCCACTTCAAGGACTGAGACTCTCTGTTGAGTCACTGAGCTCTGAGCCTA  
 GAGCCTGACACTCTCTTAAGAGGTTCTCTCAAGCCCCAAATAGCTCTCAGGGCGCCCTCGGCGGCCATCATGTGT  
 TAATTCTGTCAACAAACACACACCGGATGATGTCTGCTCTGTTGAGTGTGAGGACACAGATGACCGGACTG  
 GTCACTCTCTGCTCAACATTCAGTCTGGTATGTGAGGCGTGTGAGGAGCAAGAACTCTGGAGCTACAGGGA  
 GGGAGCCATCACTCTCGCTGGGACTCTGGAAGACTTCTGCAAGGACTCAGGCTTCAATCTTGAATCTGAAGAT  
 GTTGAAGGATGTTCTTTTACGTACCAATTCTTTGTCTTTGATATTAAAGAGAGTACATGTTCATTGTGAGAA  
 ATTTGGAACCTGTGAAGAGGATCAAGAAGAAAAATAAAATCAGCTGTGTGATATCGCTGACAAAGAAAAA  
 AA

0978585-201601

## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921  
<subunit 1 of 1, 693 aa, 1 stop  
<MW: 77738, pI: 8.87, NX(S/T): 7  
MTPQSLQLQTTLFLLSLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYKGRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRDQLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTPVVLTFQHQLQPKNVTLCQVFVVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMMVSSVEVDVAVHKHYLSLLSYVGCVVSAALACLVITIAAYLCSRVP LPC  
RRKPRDYTIKVHNNLLLAFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLTCLSWMGLE  
GYNLYRLVVEVFQTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPI ILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGLFIWIWWSMRLQARGGPSPLKNSDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

## FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTCCTGTCAACATGG

090700Z FEB 60  
FM JCRC  
TO 01-100

# FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCAGGTTTTCGCTTGA  
 TCCTTTTCAAAAACCTGGAGACACAGAAAGAGGCTCTAGGAAAAAGTTTGGATGGGATATGTGGAAACCTACCTC  
 GCGATTCTCTGCTGCGAGACAGGCTCGGCGCTTCCACCCAGTCGACGCTTCCCCTGGCGGTGGTGAAGAGAG  
 TGGGGATCGCTGCTTCCAAAGTGC CGCGCTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCCTCTTCGGGC  
 TTCTCTGCTGACATCTGCCCTGGCGGGCCAGAGACAGGGGACTCAGGCGGAATCCCAACCTGAGTAGTAAATTC  
 AGTTTTCCAGCAACAAGGAACAGAAACGAGTACAGATCTCAGCATGAGAGAATTTACTGTGTCTACTAATG  
 GAAGTATTCAACGCCCAAGGTTTCTCTACACTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
 AGGAAATGTATGGATCAACTTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAAATGACATATGCAAGT  
 ATGATTTTGTAGAAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCG  
 GAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTGTAACCCAGGT  
 TCTGCATCCACTACAACATTGTGATGCCAATTCACAGAAGCTGTGAGTCTTCAAGTCTACCCCTTCAGCTT  
 TGCCTATGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGAAGCTTATTCGATATCTTGAACCG  
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAATCTGGCAACTCTTGGCAAGGCTTTGT TTTGGAA  
 GAAATCCAGAGTGGTGGATCTGAACCTCTTACAGAGGAGGTAAGATTATACAGCTGCACACTCGTAACTTCT  
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG  
 GTGGGAACCTGTGCTGTTGTCTCCACAATTCGAATGAATGCAATGTGTCCCAAGCAAAGTTACTAAAAATACC  
 ACGAGGTCCTTCAGTTGAGACCAAGAACCGGTGTGCGAGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGACTGTGTGCGAGGGGAGCACAGGAGGATAGCCGATCACCCAGCAGCTCTTGCCCA  
 GAGCTGTGCGATGCGAGTGGCTGATTCTATTAGAGAACGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTGTCT  
 TCAAGGACCTTTTATCTCTCAGGATTTCAGTGCAATCTGAAAGAGGAGACATCAACAGAAATAGGAGTTGTGCA  
 ACAGCTCTTTTGAAGAGGAGGCTAAAGGACAGGAGAAAAGGCTTCAATCGTGGAAAGAAATTAAGTTGTGAT  
 TAAATAGTACCCAGCTAGTTTTCAGAGTTACCATGTACGTATTCACATAGCTGGGTCTCTGTTTTCAGTTCTTTTC  
 GATACGGCTTAGGGTAAATGTGCTAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGATTGGCTTGCCTTAA  
 TCTAAAGCTCCATGCTCTGGGCTTAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTGTCTCATATTCACAT  
 ATGTAAACAGAACATTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTGCTATGAATTAATTTGT  
 GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAAGAGACTACA  
 TTTATGTTTGGAAAGTATTAATATCTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTCT  
 AAACACAATTTGTATAGCCAGAGGAACAAAGATGATATAAAATATTGTGCTGCACAAAAATACATGTATTTC  
 TTCTCCATGTGTGCTAGAGTTAGATTAACTGCAATTTTAAAAAATCTGAATTTGGAATAGAAATTTGGTAAAGTTGCAA  
 GACTTTTGAATAATTAATATATCATATCTTCCATTCTGTTATGGAGATGAAATAAAAAAGCACTTATGA  
 AAGTAGACATCAGATCCAGCCATTAACCTATCTCTTTTGGGGAAATCTGAGCTAGCTCAGAAAAACAT  
 AAAGCACCTTGAAGAAAGCTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGAGTAGGAAACACATCTTATTA  
 TTGTGATGTGTGGTTTATTATCTTAACTCTGTCCATACACTTGTATAAATACATGGATATTTTATGTACA  
 GAAGTATGTCTCTTAAACGGTCACTATTGTGACTCTGGCAATTTAAAGAAAAATCAGTAAAAATTTTGTGTGT  
 AAAATGCTTAATATGTGCTAGGTTATGTGTGACTATTGAAATCAAAAATGTATTGAATCATCAATTAAGAA  
 ATGTGGCTATTTTGGGAGAAATTAAGAAAAAAGAAAAAAGGTTTAGGATAACAGGGTAAATCGCGCC

09/26/96 10:50:01

## FIGURE 207

MSLFGLLLLSALAGRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAEENVWIQLTFRFGLDEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRKSRVVDLNLLEEVRLY  
SCTPRNFVSISIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPKVKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSGTGG

**Signal sequence:**

amino acids 1-14

00070000 101001



# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACTCTCATGCTCTGCTCTCTTCAACGAGACCTCTACATTCCATTTTGGGAAGA  
 AGACTAAAAATGGTGTCTTCCAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATATCTCTAATTTTC  
 AAATCTCCTTGGGGCTAGATGGTTTCTTAAACCTCTGCCCTGTGATGTCACTCTGGAGTGTCCAAAGAACCATATG  
 ATCGTGGACTGCACAGCAAGCATTTGACAGAAATTCCTGGAGGTATCCACAGAACACCCAGAACTCACCCTC  
 ACCATTAAACACATACACAGACATCTCCCCAGCGTCTTTACAGACCTGGACCATCTGTAGAGATCGATTTCAGA  
 TGCACCTGTGTACTATTCCATCGGGTCAAAAAACACATGTGCATCAAGAGGCTGCAGATTAAACCAGAAAGC  
 TTTAGTGGACTCACTTATTTAATAATCCCTTACCTGGATGGAACACGCTATGTATGTTCATTATCAATAGAGAA  
 AACATAGAAATACTCTTACCTGGGCCAAAACCTGTATTATCGAAATCCCTGTATTGTTCATTATCAATAGAGAA  
 GATGCTCTCTTAACTTGACAAAGTTAAAGTGTCTCTCCCTGAAAGATTAACATGTACACAGCGTCCCTACTGTGT  
 TGTCCCTTACTTTTAACAGAACTATATCTCTCAACAAACATGATTGCAAAAATCCAAAGAGATGATTTTAATAAC  
 CTCAACCAATTACAAATTTCTGACTTAAGTGGAAATGCGCTCGTTGTATAATGCCCATTTTCTTGTGGCGCG  
 TGTAAAAATTAATTTCTCCCTACAGATCCCTGTAAATGCTTTGTATGCGCTGACAGAAATTAAGAGTATTTTACGTCTA  
 CACAGTAATCTCTTTCAGCATGTGCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
 CAAAACCTCTTGGCCAAAGAAATGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCCTCATCCAATTGGATCTG  
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCAACAGCATTTTCTTCACTGAAAAGCCTG  
 AAAATTTCTGGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACTCTCGGCCATTACATAATCTTCAA  
 AATCTTGAAGTTCTTGTATCTTGGCACTAACTTTATAAAAAATGTCAACCTCAGCATGTTTAAACAAATTTAAAGA  
 CTGAAAGTCTATAGATCTTTTCAGTGAATAAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTCTTGCTCAAT  
 GCCAGAACTCTGTAGAAAGTTATGAACCCAGGTCCTGGAACAATTACATTTTTCAGATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTCTTCTCATGTCTGTTAATGAAAGCTGTCAAGATATGGGCGAGCC  
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTCTTCTCTCAATGCTCTG  
 AATCTGTGAGGAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGACTGAGATATTTTG  
 GACTTCTCCAACAACCGGCTGATTACTCCATTCAACAGCATTTGAAGAGCTTCAACAACCTGGAAGTTCTGGAT  
 ATAAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTATGTCTAACTTTACCAAGAACTTAAAGGTT  
 CTGCAGAACTGATGATGAACGCAATGACATCTCTTCTTCAACAGCAGGACCATGTGAGAGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGGAATCAGTATAGTGTTTTATGGAAGAGAGGTTGATAACAGATCTTCAATATTTCAAG  
 AATCTGCTAAATATAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCTTCTGAGATTTTGTATGCT  
 ATGCTCTCAAAATCTAAGAAATCTCTTCTTGGCCAAAATGGGCTCAAACTTCAGTTGAGAGAAATCCAGTGT  
 CTAAAGAACCTGGAACCTTTGGACCTCAGCCAACCAACTGACCACATGTCCTCGAGAGATTTTCAACTGTCTCC  
 AGAAGCCTCAAGAACTGTGCTTTTGAATATAATCAATCAGGAGCTCAGGAGATTTTCTACAGATGCTCTC  
 CAGTGTGAGATATCTGATCTCAGCTCAAAATAAAATTCAGATGATCCAAAGACCACTGTAAGTATTTTCTACAGATGCTCTC  
 AAGCAATCTGAGGATGTTGCTCTTTGATCATATAATCGSTTTCTGTGCACTGTGATGCTGTGTGGTTTGTCTGGTGG  
 GTTAACCAATACGAGAGTGAATATTCCTTACCTGGCCACAGATGTGACTGTGTGGGGCCAGGAGCAACAAGGGC  
 CAAGGTGATCTCTCTGATCTGTACACTGTGAGTTAGATCTGACTAACCTGATTCTGTCTCACTTTCCATAT  
 TCTGTCTCTCTCTTCTCATGGTGTATGATGACAGCAAGTCACCTCTATTCTTGGGATGTGGGTATATTACCAT  
 TTTCTGTAAGGCCAAGATAAAGGSGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTTGTGAT  
 GACATCTAAGACCCAGCTGTGACGAGTGGGTTTGGCTGAGCTGTGGGCCAACTGGAAGACCCAAAGAGAGAA  
 CATTATTAATTTATGCTCTCGAGGAAGGGAGTGGTTTACCAGGGCAGCCAGTCTGGAAGAACTTTCCAGAGACATA  
 CAGCTTAGCAAAAAGACAGTGTGTTGATGACAGACAAGATGCAAAAGACTGAAAATTTTAAAGATAGCATTTTAC  
 TTGTCCCATCAAGCTCTGATGATGAAAAGTTGATGTGATATCTTGAATTTCTGAGAAGCCCTTTCAAGAG  
 TCCAGTGTCTCAGGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCAAACAAACCCGACAGCTCAC  
 CCACTCTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATATGACAGTGTTCAGGGA  
 ACGTCTTAGCCTTCTTTCGAAAACAACCTGCGCTAGTTTACCAAGGAGAGGCTGCG

09973585.101501

## **FIGURE 209**

MVFPMWTLKRQILILFNIIISKLLGARWFPKTLPCDVTLDVDPKNHVIDCTDKHLTEIPGG  
IPTNTNTNLTLTINHIPDISPASFHRLDHLVEIDFRNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIBILYLGQNCYR  
NPCVVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFCAPCKNNSPLQIPVNAFDALTELVKVLRLHSNLSQHVPFRWF  
KNINKLQELDLSQNFLLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKL  
KILIRIGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPIAELRYLDFSNNRLDLLH  
STAFEEHLKLEVLDISSNSHYFQSEGIHMLNFTKNLKVQLKMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSKLNLLKNNQIRSLTKYFLO  
DAFQLRYLDLSSNKIQMKTSPFENVLNNLKMLLLHHNRFLCTCDVAVFVWVNVNHTVETIP  
YLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPQGQPVLENLSQSIQLSKKTVMFMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPIFWQCLKNALATDNHVAYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

007855-10601

# FIGURE 210

GGGTACCATCTTCTGGCTGCTGCAAGTTACGGAATGAAAAATAGAAACATGGAAAAATGTTCTTC  
 AGTCGTCAATGCTGACCTGATTTTCCCTGCTAAATCTGGTTCTGTGAGTTCTGCGCGAAGAAAAATTTTCTA  
 GAAGCTTATCTTCTGTGATGAGAAAAAGCAAAATGACTCAGTTATGCGAGAGTGCAGCAATCTGCTGACTACAGGAAG  
 TTCCCAAAACGGTGGGCAAAATATGACAGAACTAGACCTGTCTGATAAATTTCACTACACATACGAATGAAT  
 CATTTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACAGAAACGGAATC  
 CCGGTATACCAATCAAAATGCTTGAATATCAAGACGGGGCATTCCTCAACCTTAAAAAATCCTTAAGGGAGTTATGTCG  
 TTGAAGACCAACCGATTGCTCCCAAAATCCCTCTGGTTTGGCAGAGTCTTTGACAGCACTTAGTCTTTTCAAAAACA  
 ATATATACCAACATTAAGTCAAGAGGGGCATTTCAAGACTTATAAACTTGAATAATCTCTTATTTGGGCTGGAACTGCT  
 ATTTTACAAAGTTTGGCGAAGAAATTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
 CACTATCTTTCAATCTCTTTTACACAGTGCACCACCAAACTGCGAAGCTCCCTACGCAAACTTTTCTGAGCAACA  
 CCGAGATCAAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACTATTACATAGATTAAAGCGGAATC  
 GTCCGAGGTGCTTCAATGCCCACTTTCCATGCGTGCCTGTGTAGTGGTGGTGCTTCAATTAATATAGATCGTTTTG  
 CTTTTCAAACTTGACCCAACTCTCGATACCTAAACCTCTCTAGCACTCCCTCAGGAAGATTAAATGCTGCTCGT  
 TTAATAATATGCTCATCTGAAGGTGCTGGATCTTGAATTTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
 TTTTAAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTAACTATAAAGGGGAGATTATCCACAGCATA  
 TTAATATTTCCAGAACTTCTCTAAACTTTTGTCTCTAGGGCATTTGATTTAAGAGGTTATGTTTCCAGGAAC  
 TCAGAGAAAGATGATTTCCAGCCCTGATGCAGCTTCCAACTATTCGACTATCAACTTGGGTATTAATTTTATTA  
 AGCAAAATCGATTTCAAACTTTTCCAAATTTCTCCAATCTGGAATATTTTACTGTGAGAAAAACAGAAATATCAC  
 CGTTGGTAAAGAGATACCCGAGAGGATTATGCAAAATAGTCTCTCTTTTCCAGTGCATATCCGGAACAGCAGCTCAA  
 CAGATTTTGAAGTTTACGCCCACTTGAACCTTTTATCAATTTCAACCGTCTTTTAAATAAGCCCAATGTGCTGCTT  
 ATGGAAGAGGCTTGAATTTAAGCCTCAACAGTATTTTCTTCAATTTGAGGCAACCAATTTGAAATCTTCTGTGACA  
 TTGCTGTGTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAATCAATTTTCAAGCAATCTCTCATG  
 TCAAAATATTTGGAATTTGCAAAATAGACTAGACTTGTAAATGTAGTCTTACTGAAATTTGCTGCACTTGG  
 AAGTTCTAGATCTCAGCTATATAATTCACATATTTAGAAATAGCAGGGCTAAACATATATAGATTTATTTCAA  
 ATTTTCAAAATCTAAAAGTTTTTAACTTTGAGCCACAAACCAATTTATCTTTAAACAGATAGTATAACCTGGAAA  
 GCAAGTCCCTGTAGGATATAGTTTTCAGTGCAATCGCTTGCATTTTGTGGAATGATGATGACACAGGATTA  
 TCTCCATTTTCAAAGGATCTAGAAATCTGACACGCTCGGATTTATCCCTTAAGTGTGAGCAATCTCCAAATG  
 AAGCATCTCCATAATTTGCCAGCAGTCTCACTGACTATCATATAATGATAATGTTTAAAGTTTCTTAACTCGGA  
 CATTTACTCCAGCAAGTTTCTCGTCTCGAGTGTGACTGACTGCGAAACAACTCTCTTTTAACTCGCATGCC  
 TATCTGACTTTTACATCTCCCTCTCGACACTGCTGCTGACTATAACAGGATTTTCCCACTTACCCTTGGCTTTC  
 TTTTGAAGTCAAGTGTGATGATGACACTCGAATTTAAGTTTCAATCTGCTAAAACCAATCAACAACTCCGACTTTG  
 AAACATAGACACCAACCAATTTATCTATGTTGGAATACACGGAACCCCTTGAATGCACTCTGATCAATTTGAG  
 ATTTCCGAAGATGATGATGACACTCGAATGTCAAATTTCCAGCACTGGTAGATGCTATTTGTGCGCACTCGT  
 GGGATCAAGAGGAGGAGAGATTTGTGAGTCTGGAGCTAACAACTGTGTTTCAAGTGTCACTGCAAGTATTTAT  
 TTTTCTCAGCTTCTTTATCACCACTGGTTATGTTGCTGCTGCTGCTCACCATTGTTTCTATGCGGATGTTT  
 TTTTATATATAATGTGTGTTTGTAGCTAAGGTAAAAGGCTACAGGCTCTTTCCCACTCCCAAACTTTCTATGATG  
 CTTACATTTCTATGACACCAAAGTGCTCTGTACTGACTGGGTGATAAATGAGTCTGGCTACCACTTTGAAG  
 AGAGCCGAGACAAAAACGTTCTCTTTGTCAGAGGAGAGGATTTGGACCCGGGATTTGCCATCATCGACAAC  
 TCATCCAGACATCAACCAAAGCAAGAAAAAGTATTTGTTTAAACAAAAAATATGCAAAAAGCTGGAACTTTA  
 AAACAGCTTTTATCTGGCTTTGCAAGGCTAATGGATGAGAACATGGATGTGATTTATTTATCTCTGTGGAGC  
 CAGTGTATCAGCATCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCTCCAGTGGGCTGACA  
 ACCGGAAGGCAGAGGCTGTTTGTGGCAAACTCTGAGAAATGTGGCTTTGATTTATTTCTGAGTATGA  
 ATATGTATGTCGATTCATTAAGCAATACTAAGTACGTTAAGTCATGATTTTCGCGCCATAATAAGATGCAAG  
 GAATGACATTTCTGATTAGTTATCTTATGCTATGTAAACAAATATCCCAAACTTAGTGGTTTAAACAAACACA  
 TTTGCTGGCCCAACAGTTTGTGAGGCTCAGGAGCTCAGGCCCCAGCATAACTGGGCTCTCTGCTCAGGGTGTCTAG  
 AGGCTGCAATGTAGGTGTTTCAACAGAGCATAGGCATCACTGGGCTCACAATCTGATGTGGTTGTTTCTGAGTTCA  
 ATTCCTCTCGGCTATTTGGCCAAAGGCTATCTCATGTAAGCCATGCGAGCTCTCCCAACAGGCGAGCTTGCTTC  
 ATCAGAGCTAGCAAAAAAGGAGGTTGCTAGCAAGATGAAGTCAAACTCTTTGTAATCGAATCAAAAAAGGAT  
 TCTCATCATCTTTGGCCATTTCTATTTGTTAGAAATGAAACCAAGTCCCAAGCTCCATGAGGAGTGACCA  
 CAGTCTCAGGGAAACACCTGAAGACCAAGATGGTGAAGTCTGATGCTGATGCTGATGCTGATGCTTTCCCT  
 TGACTGTGCTGCTGGGATGGCTGCTATCTGATGATAGATTGTGAATATCAGGAGGCGAGGATCACTGTGGAAC  
 ATCTTAGCAGTGTGACCTAACACATCTTTTCAATATCTAAGAACTTTTGGCACTAGCTAATAGTGTCTAATA  
 TTAAGCTGTGTTTATATTTATCATATCTATGGCTACATGTTATATATGCTGTGGTGTGGTTCGGTTTTAT  
 TTACAGTGTGCTTTTCAAAATTTTCTGTAACATTTGACTTCTAAGGTTTAGATGCAATTTAAGAACTAGATGG  
 ATAGCTTTTAAAGCATCTTTTACTCTTCAACATTTTAAAAGATGACAGCTTAAATCTGAAGCTTTTGGTCTATA  
 TTGTTAATGGCAATGCTGTAAATCTTAAATGAATGAATAAAATGTTTCACTTTTACAAAAAATAAAAAA

00978535.101601

## **FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPYCDKQNDSVIAECNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNNGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLLSLSPNSLSHVPPKLPSSLRKLFLSNTQIKYI SEEDFKGLINL  
TLDDLSGNCPRCFNAPPCVPCDGGASINIDRFQNLTLQLRYLNLSSLSLRKINAAWFKNM  
PHLKVLDELFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSNRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFFEDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWDDDNRYISIFKGLKNLTRLDLNLRKHIPNEAFLNLPASLTELHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLSHNRISHLP SGFLSEVSSLKHLDLNLS  
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFFITTMVLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGFLWQTLRNVVLTENDSRYNMYVDSIKQY

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 826-848

## FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC  
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCAACCCGGAGGA  
GCAGTCTCTGCCCTGTCCGGGGGATGACTGATTCTCTCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGTGTGTGATGTGGCTT  
CTGGTGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGTGT  
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTCTGCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCTATGCCGAACGGAGGGA  
GCTGTGTCCAGCTGGCCGCTGCCCTGCAGGATGGCGGGGTGACAGTTGCCAGTCA  
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCACTGCACAGCCTGGCCTGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCTGAGCGAGCAGATTTCTTCTCTG  
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCGCGCCTGCAGCCCCATGCCCTGCCCAACATGTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCC  
TTCTCTGGGAGGCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCCGAG  
GCTGGGTGGGGCTCAGTGGGGGCTGCTGCCTGACCCCGCAGCACAATAAAATGAAACGTGA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCGCGCACTCTAGAGT  
CGACCTGCAGAAGCTTGGCGGCATGGCCCAACTTGTTTATGTCAGCTTATAATGGTTACAAAT

007525.10101

## FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLITCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09070535.101601

## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCACGCGGGGCCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCTGTCTCCGAGTCTGTTCCG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGAGCCTTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGTGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGGTGCACCTCTCCAGCAGCTCGGCCCGATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTCTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAGGCTCCCCAGACCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCTGGCTACCCCCAAGGCA  
TCCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGAC  
CCCCAGCACAATAAAAAATGAAACGTG

**FIGURE 215**

MRGSQEVLLMWLLVLVAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPLFTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACPCPGWKRTSGLPGACGAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTCCQSDVDECSARRGGCCPCRCINTAGSYWCQCWEHGSLSADGTLCPVKGPPRVA  
PNPTGVDSAMKEEQLQRSRVDLLEKLLQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLG  
RIDSLSEQISFEEQLGSCSCCKKDS

**Signal sequence:**

1-19



CCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCCTCAGGCGGCCAGTGGGCCTGAGGCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGCTCCAGCAGCAT  
CAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCG  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTCTGTGTTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCTGTCTCCGAGTGTTCGTGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC  
GGGACACGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCTACCGCCGAGCCCTGG  
GCTGGCCCTGCCAGGCTCGCTACGCGTGTGCCCCGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGCTCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGTGCCTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG  
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGTGGTGTGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC  
TTCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTCTTGAGGAGCAGCT  
GGGTCCTGTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCAGCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCG  
GGTGAGCTGAGCGGAAGGCACAGGCAGGGCCTTCTCTCTTCTCCTCCTCCTCGGGAG  
GCTCCCCAGCCCTGGCACTGGAGTGGGCTGGGATCTTCTGTGTAATCCACCCTGGCTACC  
CCCACCTTGGCTACCCCAACGGCATCCAGGCCAGTGTTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGTCTCTGTCTGGAGCTGGGACCCATGGCACAGGCCAGGCAGCCGAGGCTGGGTGGGG  
CCTCAGTGGGGCTGTGCTGCCACCCCCAGCACAAATAAAATGAAGCTG

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR  
CPAGWRGDTCCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09073585 101501  
T09073585 101501

# FIGURE 218

GGTTCACACAGCTGGTTTAGGGCCCGACCACTGGGGCCCTTGTGAGGAGGAGACAGCTCCCGGCCCGGGGAG  
 GACAAGTCGCTGCCACTTTGGCTGCGGACGTGATTCCCTGGGACGGTCCCTTTCCTGCCGTGAGCTGCCGGCCG  
 AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCCTGGTCTCCCTTCTCCCGCTGGGCCGGTATTATCGGGAGG  
 AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGAGGAATAGCAGGCCAACGTGAT  
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGGTGTAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA  
 TGTCTGTGTGTTGGTGAGAAAGAGGTGACACGGAATGGGAGAACTCCAGGCCAGGAACACTTTTGTGTGTG  
 ATGGCCCGCTCATGATGGCCCGGCAAAAGGGCAATTTCTACCTGACCCCTTTCTCATCCTGGGGACATGTACAC  
 TCTTCTTGGCCCTTGTGAGTCCCTACCTGCTGTTTCTGCTGTCCTGCCATCCCTGTATTGTGTCCTGCTCT  
 TCCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGGCTTACCAGATG  
 AAGCAGCTTTCATAGAAATGGAGATAGAACTACCAATGTTGCGGTGGCCCGAGGCCAGCAACCGCTCGTA  
 TCAAGAATTTCCAGATAAACCAACAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCTCCCC  
 GGGCTCCCATTTGACGATCTGTGACAACTGTGTGGAGCGCTTCGACCATCATGCCCCCTGGTGGGGGAATGTG  
 TGGAAAGAGGAACACCGCTACTTCTACCTCTTCATCTTCTCTCTCCCTCTCACAATCTATGCTTCGCTT  
 TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTTGAAAGAACTCCTGGAACTG  
 TCTAGAAAGTCTCATTGTCTTCTTACACTCTGGTCCGTGGGACTGACTGGATTTTACACTTTCTCGTGG  
 CTCTCAACGACACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATGCGCTCCAGATCCCTACAGCC  
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTCTGTGGGCCCTTGGCCCCAGTGTGCTGGATCGAAGGGGT  
 TTTTGGCACTGGAGGAAGTGAAGTGCAGCTCCAGTACTCAAGAGACAGTAGCAGCTCTTGGCCACAGAGCC  
 CAGCCCCACAGAACACTGGAATCAAAATGAGATGCCGGAGGACAGCAGCATCCCGAAGAGATGCCACCTCCAG  
 AGCCCCAGAGCCACCAAGGAGGCGAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTGTTTGTGTT  
 TAATTAGGCTATGAGAGATTTGAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAGCTGTCCCTTTTAACT  
 GTTTTCTTGTGCTTTAGTCAACCCAGTGTGACACTGGCATTCTTCTGTGCAAGCTTTTAAATTTCTGAACT  
 CAAGGCGAGTGGCAGAAGATGTGACTGACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTCT  
 CCAATGGCTCAGCCACAGGGTCCCCCTGGACCCCTCTCTTCCCTCCAGATCCAGGCCCTCCTGTCTGGGTGAC  
 TGGTCTCATTTCTGGGGCTAAAAGTTTGTGAGACTGGCTCAAATCCTCCAGCTGCTGCACTGTCTGAGTCCAGA  
 GGCAGTCAACAGACCTCTGGCCAGGGGATCTAACTGGGTCTTGGGGTCTTCCAGACTGAAGAGGAGGAGAG  
 TGGGTTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTTGCCCAAAATCCTTTTGAATAGGGACAGGTACCT  
 TCCACTGTGTANN  
 CAGGAATGGCAGTAAATAAAGTCTGCACTTGTGCTATTCTTCTTCTCAGAGGAAGCCGAGTGTCTCACTTAAAC  
 ACTATCCCTCAGACTCCCTGTGTGAGGCTCTGAGAGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
 GCTCTCCTCTCTCTCTCTCCCCGATGTACCTCAAAAAAATGCTAAACAGTTTCTTCCATTAGGCT  
 CGCTGAGTGGGGAAGCCAGCACTGTGSCCTCTCGGGTAACTCACTTAAAGGCTCGGGCCCTCCCTCTGGCT  
 ATGGTAAACCACTGCGGGCTCTCTCAAGCCCGCTCTTCCAGACTTCCACGGCAGAGTCCCAAGAGCCATGT  
 CACCTTGGGGGTGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAGATTATGT  
 ATTATATGTGCTATATTTCTAGAGCACTGTGTTTCTCTTTCTAAGCCAGGGTCTGTCTGATGACTTAT  
 CGGGTGGGGAGTGTAAACCGGAATTTTCATCTATTGGAAGCGATTAACTGTGCTCTAATGCA

097355.101601

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGNCGKRNRYFYLYL  
FILSLSLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI CFFTLWSVVGLTGFHTF  
LVALNQTTNEDIKGSWTGKNRVQNFYSHGNIVKNCCEVLCG PLPSPVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEA AEAEK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

00733-10101

## **FIGURE 220**

AAAACCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTNTTCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCTGGGTGGGGAATTGTGTTGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTINTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

09070533 101501

**DEPARTMENT OF THE ARMY**

GTGTGTCTCCTTCAGCAAAAAGTCAGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGCACAAAAAGAGAAAAAGAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCATATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA  
CAAGTGGTGCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGAC  
GAATACTTTGAAATTCAGGGCATTACC CGGGAGCAGT CAGGGGACTACGAGTGCAGTGCCCTC  
CAATGACGTGGCCGCGCGCTGGTACGAGAGTAAAGGTACCGTGAATCTCCACCATACA  
TTTCAGAAAGCAAGGGTACAGGTGTCTCCCGTGGGACAAAGGGGACACTGCAGTTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAGGATGACAAAGAAGCTATTGAAGGAAA  
GAAAGGGGTGAAAGTGAAAAACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTG  
AACATGACTATGGAACTACACTTGGTGGCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAGAAATTGAA  
AATTGCCCTTGAGATATTTAGGTACAATGGAGTTTTCTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
GATCTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGGCCAAGCGTGGCGCTGCGG  
GCATCTTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## **FIGURE 222**

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECSASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML  
FGPGAVSEVSNGTSSRRAGCVWLLPLLVLHLLKF

**Signal peptide:**

amino acids 1-28

0070225 104501

## FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGCTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

09073235-101601



**09-06-2017**

ATGGCTGTGTGACGGCGGGGCGGGGACAGGGGACCGGGGGCGCGCCGGAGCGGGCGAGCTCTCGGGAGCGCTTGA  
ATACCGCTCGGCGCCGATCCACCACTAGCACTGCGCTCGAGGAGCTGGGAGCTGGCAGCAAGCTGGGAGATTCGAG  
AAGGGAACGACAGACAGCTGTATTAGCTCCAGCAGCGAGCTGGAGCTGGTCTTATGAGCTGGCTCTCTACTTGCTGGCT  
GCATCTCTTCTGGCTGCTCTTGTGGCGCTTACGAGGCTCCAGTACACAGAGACCCATCTCCACAGCACTTGCCTTTACA  
GAGGCTCGCATTCGAGTGGCTGGAAAATCTCGAGTGGCTCCGTCGCGAGGGGTGAGCCCTCTGTGAGGACTTTTAC  
CAGTCTCTCTGTGGGGTGAGTCTGGAGAAACCCCTCGCCAGCTGGGGCTTCTCGCTGGAAACACCTTCCACAC  
CTCTGGGACAAACCGGCGCATCTGAAGCACTGCTTGAAACACCACTTCAACTCAGCAGCTGAAGAGCTGAG  
CAGAGACACAGCGCTCTCTACTTCTTCTGCTTACAGTGGAGGACGATAGGAGAGCTGGGAGCGCCAGCCATCTGAG  
GACCTCATTGAGAAAGTTTGGTGGTGGAACTACGCGGGCGCTGGGACAGCAACTTATAGGAGTGGTTGAGG  
CGAGTGAACGAGGACCTACAGGCGCCACCCATCTTCACCTCTACATCAGTGGCGCATCTTAAGAGTCTTCCACAG  
AATGTTATTCAGGCTGGACAGCTTGGGCTCTTCTGGCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAGTGTCTCATGCTCTTCTGATTACATGAGAAAGTGGGATGCTCTGGTGGGGCGGCCCATCTCCAGGAGC  
GAGCAGATCAGCAGAGGCTGTGGAGTTGGAGATACAGCTGGCCCAATCACATGCCACCGACAGCGCGCGAC  
GAGGAGAGATCTACACAGAGATGACATTTCCGAGCTCGAGCTCTGGCGCCCTCTGAGTGCATCAGTGTGAGTTCT  
GAGTTCTTCTGTGTCACCATTTGAGTTGAGTGTGACTTGAGCTTGTTGGTGGTATGGGATGGATTTTTCGAG  
CAGGCTCAGAGCTCATCAACCGCGAGGAGACCAAGCATCTGGAACAAITACTGATCTGAGACCTGGTGTGAAGAAG  
ACAACTCAGAGCTGGAGCGAGCTTTGAGTGTGTCACAGAGAACTGCTGGAGACCTCATTGGCATAAGAA  
TCTCTGTGTGGCAGGTGGCAGCATGCACTCTCAACAGCGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCT  
GTGAAGGCGCATGTTTACCGGCAAGCAAGAARATTTGACAGGGGATGATCAGGAAATCCGAGCGCAATTTGAG  
GAGGCGCTGGGACAGCTGTTTGTGATGGATGAGAAGACCGCCAGCGACCGAAGGAGAAAGCAGATCGCACTTAT  
GATGATGATTTGGTTTCCAGACATCTCTCGAGCGCCAAAGAGCTGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATCTTTCTTCTCAAAACAGTTTGAATTTGTACAACCTTCTCTGCCAGGTTATGGCTTGACCACTCTCGCAG  
CTCCGACGCGAGACAGCTGGAGCATGACCCCGAGACAGTGAAATCGCTTACTCTTCACTTCAAGTAAAGTGAAT  
GTCTCTCCCGCTGGCATCTCTGAGCGCCCCCTCTATGCGCGCAACACCCGAGGCCCTGAACTCTGGTGGCATCT  
GGTGTGGTCTATGGGCACTGAGTTTGACGATGCTTTGTATGACAGAGGCGCGAGTATGACAAAGAAGAGGAACTCTG  
CGGCCCTGGTGCGAAGATGAGTCCCTGGAGCCTCTCGGAACACACGCGCTGCACTGGAGGAACAGTCAATCACT  
TACAGGATCAATGGGAGAGGCTCAAGCGGCGAGAGCTGGGGAGGAAACTATTGACACACGGGGGCTGAAG  
GCTGCTCTCAATGCTTACAAAGCATGCTCGAGAAGCATGGGAGAGAGCAGCACTCGACAGCGTGGGGCTCAC  
AACACACAGCTCTTCTCTGTGGGATTTGCCAGGCTGGTGTCTCGTTCGACACACAGAGAGCTCTACAGAGGG  
CTGTTGACCGACCCCGACAGGCTCGGCCCTCTCGGCTCTGGGCACTCTTCCAATCCCGTGAATCTCTTCTCGG  
CATCTTCGCTGGCTGCTCGGCTTCCCCATGAACACAGGCGACTGTGTGAGTGTGGTAGACATCTGATCAGGGA  
GAAATGGCCAGCTGTACACAGACTGGGGAGCTCTCTGACAAAGCTTTGTGCTTGGGTTGGGAGAGGACAA  
ATCAGACTGGGCTGGGTGTGATCTCCCTCCCCACAGTGACATGATGACAGCCCTCTCAATCACCACATGT  
TGCCCTCTGCTTTGGGGTGCCCTGCTCCAGCAGAGCGCCCACTTACATGTTGACATCTTTCGTGTCAACCT  
CGTGGAAAGAGTCTGGGTGGGGAGCGATCTCCATAGGAAGAGTCTGCC

## FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES�DRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA  
ILKHLLENTTFNSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGFPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPSTSTREQMQLVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTAEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVDGYEISEDSF  
FQNLNLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFQVWCS  
VRTPESSHEGLVTDPHSPARFVLGTLNSNRDFLRHFGCPVGSPMNPQLCEVW

**Type II Transmembrane domain:**

amino acids 32-57



## FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCTGGCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGTGGATTCCGA  
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAAACACTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAAACACACTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCACTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAAACTGCCCT  
CCTTTCTTTCTTCTTTTCTTCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAAGAGGTCCTGAGGATTACAGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTGAGCCAGGTCTCTGAT

347557-1004

## FIGURE 228

ATGCCTACTACCTTCCAACATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC  
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATCGGTGGTGCATGGGCCA  
TGAGTTGACGCATGCCCTTGATGACCAAGGGCGCAGTATGACAAAGAAGGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACAGCGCTGCATGGAGGAACAT  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGTCTGGCACTCTCTCAAACCTCCCGTGACTTCTGCGGC  
ACTTCGGCTGCCCTGTCTGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTTGACAAAGCTGT  
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCACA  
GGTGACATGAGTACAGACCCTCTCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCACCATTCAGTGTGACATCTTTCGCTGTACCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCTGCGGTGCTGCCCTGCTGTGACCCACAGGCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCTCAGGGCTACCCCACTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGTCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGATATGTGTAGCGGTAAGTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

09978555 104602

# FIGURE 229

CCCACGCGTCCGAGCGCCCGAGAATTAGACACACTCCGGACGCGGCGCAAAGCAACCGAGA  
 GAGGGGAGGCAAAAAACCCGAAAAACAAAAGAGAGAAACAACCCCACTGGGGTGG  
 GGGGAAGAAAGAAAAAGAAACCCACCCACCCAAAAAAGAAAAAAGAAAAA  
 AAAAAAAGAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCAGCCAGGGGG  
 TGGGGGAGTGCAGCTGAAAGCTGCTGCTGAGCAGCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGTCTTTGCTCGAACCCAGTGGCTGGCGGGCTGCTCCTCAGCCTGTG  
 CTGCTGTCTACCTCTCTGCTCCCGCTGGACAGAGTGTGACATTCCTCCTGGCGCGCTGG  
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGTGTGTTTGGGAAGATGGAGCT  
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTCGGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTGACAGTCAACATACACCCAGAACCA  
 ATGCAAGGTGCATCTAACTGTGCAAGTTCCTCTTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCTTACTTGTGTTGGCCACTGGGAACCCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGCAATATTTGGACATT  
 TATGGAATTACAGGGACCCAGGCTGGGGAATATGAATGCAGTGCAGGAAATGCTGTGTCATT  
 CCCAGATGTGAGGAAAGTAAAGTGTGTCAACTTTGCTCCTACTATTCCAGGAAATTAAT  
 CTGGCACCGTGACCCCCGGACCGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAAAGGAATATTATTA  
 TCAAAATTTTAGACACAAGATCCATTCTCACTGTACCAAGTGCACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAACAAAGCTAGGCACAACCAATGCGAGCCTGCGCTCTTAACCT  
 CCAAGTACAGCCAGTATGGAAATACCGGGAGCGCTGATGTTCTTTTCTCCTGTGGTACCT  
 TGTGTTGACACTGTCTCTTTTACCAGCATATTTCTACTGAAAGATGCTTACAAATGAAA  
 TTCAAAGACCCATAAAAGGCTTTTAAAGGATCTCTGAAAGTGTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCCTTACATGGGAGGTGATCGCC  
 TTCTGTAGAAATGCTCATTATGTAAATACCTTTAATTCTACTCTTTTTTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCTCTTTTTTAAAGAGTGAAGCTCTGAAATTACTTTTAG  
 AGGATATTAATTTGATTTTCACTGTTTGTAAATCTACAACTTTCAAAGCATTGATGATGGT  
 CTGCTAGGTTGCAAGCTGTGATTTTACAAAACGAATATGCAAGTGAATATGTGATTCTTTAA  
 GGCTGCAATACAAAGCTTCACTTCCCTGTTTCAATAAGAGTCAATCCACATTTTCAAAGATG  
 CATTTTTTTCTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATATTGCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTGTGATGATATTCAAGTTTCAAGGATGAGCCTTGTAAAT  
 ATAACCTGGCTGTGACAGCTCTGCTTCTCTTTCTGTAAGTTCAGCATGGGTGAGCCTTATAC  
 AATAATATTTTTCTCTTGTCTCCAACTAATATAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACAGAGTATCAAGTTAAACCATACTATCTCTAAGTAAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCTGCACTGACAAATGGGGTTTGAGAAATTTTGGCCCCACACT  
 AACTCAGTTTCTGTGATGAGAGACAATTTAATAACAGTATAGTAATATACCATATGATTTT  
 TTAGTTGTAGCTAAATGTGTAGATCCACCGTGGGAAATCATCTCCCTTTAAATGACAGCACA  
 GTCCACTCAAAGGATTGCTTAGCAATACAGCATCTTTTCTCTTCACTAGTCCAAGCCAAAAA  
 TTTTAAAGATGATTTGTGAGAAAGGACAAAGTCCATATCACTAATATTAACAAGATTTGGTA  
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGTATTTTATAAAGGTTTGG  
 AGCTGACCTGAAGCATCTTATTTTATAGTATATCAACCTTTGTTTTTAAATTTGACCTGCCA  
 AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTTCTGCTATTTTAA  
 AGACAAATATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 230**

MLLVQGACCSNQWLA AVL LLSL CCLLP SCLPAGQSVD FFWAAVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSII FAGGDKWSVD PRVSI STL NKR DYSLQI QNV DVTDDGPYTC SVQTQHTP  
RTMQVHLTVQVPKIIDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPVRKVKVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVL FSCWYLVLTLSSTSI FYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

0070505-101004

## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAGCTTGGCAATGAGAAAATAGAAAAATTTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATGCAATGGAGCCTTTTCGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAAATGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCTTGAGATGTATTTCCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGATCGAGGGT  
CAAGTCTGTCAGGCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGTCAGCGGGT  
AGACAACCTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGTGAAACAAGGCGCCCCAGGTC  
TTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTTCGGGACCCCAAG  
CCACCGGGAGTCAAGGGAGAGCGGGCCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCGAGGACCCCAAGGAGAGAAAGGCGAGCAAAAGCGATGGGGGTCTCAT  
GGCCCCAAAAGGGGAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGTTCATGGGGCTCTGGAGCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGAAGTGCAGGGTGTTCGGGGCCCTCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGTGAGCCTGGCAGTGTCTGGTCCCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGGAGAACAGGGGAGCCAGG  
GCTGGCAGGTCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAATCAGTGTCC  
GTCAGGATTGTTCGGCAGTAGTAACCGAGGCCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAAGTGTTCGGGACAGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGACTCAGGCCACGAGGAGGACGCGAGCGTGGAGTGCAGCGTCTGAACCCGGAACCCCTTCA  
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAAGCTCAACATCATTGA



## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPQGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPAEKGAKGAMGRD  
GATGPGSPQGPPGVKGEAGLQGPQGAAPGKQATGTPGPQGEKSGKDGGLIGPKGETGTKGE  
KGDLLGLPGSKGDRGMKGADAGVMGPPGAQGSKGDFGRPGPPGLAGFPKAGKDGQGPGLQGVPG  
PPGAVGHHPGAKGEPGSGAGSPGRAGLPGSPGSPGATGLKGSKGDTGLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEGGQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWTGTICDDEWQNSDAIVFCRMLGYSKGRALYKVAGTGQIWLNDNVQCRGTSTLW  
SCTKNSWGHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

0344/bk66-27 at 112, 113, 114, 115

CCCACGCGTCCGAAGGCAGACAAAGGTTTCATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGGCCAAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAGGAAGAAGAAGAAAAGGGCCAAAGCCTAAAGTGAAGCTGATGGTACTTGTTTTCAC  
CATTGGGTAACTTTGTCTGTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCAAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG  
TGATTCCTTGCAACAATCAATGGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC  
CCACAAACTCAGACTACATCAGTATAAATGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATCTTATAAATCTTCTATGTCTTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAATAAAAAA

## **FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758  
<subunit 1 of 1, 98 aa, 1 stop  
<MW: 11081, pI: 6.68, NX(S/T): 1  
MKLMVLVFTIGLTLLLGVOAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG  
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

**U.S. DEPARTMENT OF AGRICULTURE**

CCACGCGCTCCGCGGACGCGTGGGCTGGACCCAGGTCCTGGAGCGAAATTCAGCCTGCAGGGCTGATAGCGAGGCATTATGAGATGTGAGAGACACTTACCCCGCGCTGGTGGTGGAGGGCGCGATAGAGCAGCAGACGACGGCGGGTCCCGGGAGCGCGCTGTCTGCCTCGCCAGATGTGGATATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCCGCGCTGGCTGTGCGCTGGGCGCTGGTGTCTGGCGGGTGGCTTCTTCTCCTCGGCTTCTCTTCGGTGGGTTTATAAAATCTTCCAATGAAGCTATCAACATTACTCCAAAGCATATATGAAGACATTTTGGATGAATTTGAAGAGCTGAGAACCATCAAGAAGTTCTACATAATTTTACAGATACCAATTTAGCAGGAACAGAACAAATTTTTCAGCTTGCAAGACGATCAATCCCGAGCTGGAAGAATTTGGCTGGATTTCTGTTGAGCTAGCTCATTATGATGTCTGTGTTGCTTACCCTAACCTACCTCCGAATCATCCGAACTCACTCATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTAATTTGAACCACCTCCAGGATATGAAAATGTTTTCGAGATATTGTACACCCTTTCACTGCTCTTCTCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTTAACTATGCAAGCACTGAAGACTTTCTTAAATTTGGAACGGGACATGAAATCAATTTGCTCTGGGAAAATTTGTAATGCCAGATATGGGAAGTTTTCAGAGGAAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGATGCATTTCTACTCCGACCTCGTACTATCTTTGCTCTGGGGGTGAAGTCCCTATCAGACGGTGTGAATCTTCTTGGAGGTGGTGTCCAGCGTGGAATATCTTAAATCTGAATGGTGAGGAGACCTCTCACACCAAGGTTCCAGCAGAAATGAATGTCTTATAGCGCTGGAATTCAGAGGCTGTTGGTCTTCCAAATTCCTGTTTCAATCCAAATTTGGATACTAGTGCACAGAGCTCTTGAAAAAATGGGTTGTCAGCACCACAGATAGCAGCTGGAGAGAAGTCTCAAAGTCCCTCAATGTTGGACCTGGCTTTACTTGGAAATCTTTTCTACAAAAAGTCAAGATGCATCACTTCCTACCAATGAAGTGAACGAAATTTCAATGTGATAGTACTCTCAGAGGAGCAGTGGAAACAGACATATGTCAATTTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAGCAGCTGTGTGTTTCAATAAATTTGGAGGACTTTTGAACATCGAAAAGGAAGGTTGGAGACCTTGAAGAAACAATTTTGTTCAGCTGGGATGTGCGAGTATGCAAGAAATTTGGTCTTTGTGTTCTAGTGGGCGAGAGAAATTCAGACTCTTCAAGAGCGTGGCGTGGCTATGATTAATGCTGACTCATCTATAGAAGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACCATAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTCTTTATGAAGTTGGATAAATAAAGCTCTTCCAGAGTTCAGTGCAATGCCCAGGATAAGCAAAATGGGATCTGGAAATGATTTGAGGTGTTCTTCCAGCACTTGAATTTGCTTCAGGACAGCAGCGTATATAAAAATTTGGGAACAACAAATTTACGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGTGGGAAAAGTTTATGATCCAATGTTTAAATATCACTCTACTGCTGGGCCAGGTTGGAGGAGGATGGTGTGAGCTAGCCAAATTCATAGTGCTCCCTTTGATTGTGAGATATGTCTGATGTTTGAAGAGTATGCTGCAGAAAATCTAAGATTTCTATGAGTATTTAGATATGCTGCAGAAAATCTAAGTATTTCTATGAACATCCACAGGAAATGAAACATACAGCTGTATCTATTTGATCACTTTTTTCTGCAGTAAGAATTTTTACAGAATTGCTTCCAAAGTTCAGTGAGAGACTCCAGGACTTTTGACAAAAGCAACCCAATGATATTAGAAATGATGAATGATCAACTGATTTCTGGAAGAGCATTTATGATCACTTAGGTTTCCACAGAGGCTCTTTATAGGATGCTATCTATGCTCCAGAGCCACAAAGTATGCAGGGAGTCAATCCAGGAATTTATGATGCTCTGTGATGCTTCAAGGCTTTCAGGACAGATTTATGATGCTCTGTGTAATTTGAAAGCAAGTGGACCTTCCAAAGGCTGGGAGGTGAAGAGACAGATTTATGTTGCAAGCTTCAAGTGCAGGCGAGCTGCAGAGACTTTGAGTGAAGTAGCTCTAAGAGGATTTTTAGAGAATCGTATGAAATTTGTGGTATGTCTACAGAAAGATCGTATGGGTATTTGATAAATTTTAAATTTGGTATATTTGAAATAAAGTTGAAATTTATATATAA

## FIGURE 236

>/usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756  
><subunit 1 of 1, 750 aa, 1 stop  
><MW: 84305, pI: 6.93, NX(S/T): 10  
MWNLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAF  
DELKAENIKKFLHNFTQIPHLAGTEQNFLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH  
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGLVYVNYARTEDFF  
KLERDMKINCSGKIVARIYRGKVFGRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWN  
PGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPD  
ILGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW  
AEENSRLQERGVAYINADSSIEGNYTLRVDCPTPLMYSLVHNLTKEKSPDEGFEGKSLYES  
WTKKSPSPFSGMPRIKSLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSHVET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLFPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTYSVSFDLSLFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAAE  
TLSEVA

### Signal sequence:

amino acids 1-40

### N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

### N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713